

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run On: November 30, 2002, 04:09:48 ; Search time 2080 Seconds  
(without alignments)  
3425.968 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgacttc.....ggaaatnntagataaaaaant 440

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 267.6 | 60.8        | 974    | 11 | AY108359 Zea mays  |
| 2          | 266.6 | 60.6        | 492    | 10 | AW424591 707018G10 |
| 3          | 258.6 | 58.8        | 646    | 14 | BQ487045 1091050G1 |
| 4          | 246.6 | 56.0        | 491    | 9  | AI948185 603037E02 |
| 5          | 225.2 | 51.2        | 583    | 10 | BE553166 946089H09 |
| 6          | 222.8 | 50.6        | 511    | 13 | BI233723 949032B03 |

|    |       |      |      |    |          |
|----|-------|------|------|----|----------|
| 7  | 218   | 49.5 | 531  | 10 | AW925193 |
| 8  | 217.4 | 49.4 | 508  | 11 | BE552951 |
| 9  | 217.4 | 49.4 | 991  | 10 | AY104688 |
| 10 | 169.2 | 38.5 | 243  | 10 | BE511251 |
| 11 | 127.2 | 28.9 | 450  | 9  | AL822592 |
| 12 | 126.6 | 28.8 | 453  | 17 | BH217843 |
| 13 | 126.4 | 28.7 | 603  | 10 | BE404891 |
| 14 | 126.4 | 28.7 | 791  | 14 | BQ483893 |
| 15 | 125   | 28.4 | 1206 | 10 | BE421015 |
| 16 | 124.8 | 28.4 | 460  | 12 | BE904016 |
| 17 | 124.8 | 28.4 | 486  | 10 | BE499155 |
| 18 | 124.8 | 28.4 | 500  | 10 | BE405417 |
| 19 | 124.8 | 28.4 | 535  | 12 | BE904017 |
| 20 | 124.8 | 28.4 | 535  | 12 | BE909866 |
| 21 | 124.8 | 28.4 | 571  | 13 | BM134936 |
| 22 | 124.8 | 28.4 | 596  | 10 | BE500781 |
| 23 | 124.8 | 28.4 | 733  | 14 | BQ579753 |
| 24 | 124.2 | 28.2 | 557  | 13 | BM375207 |
| 25 | 123.6 | 28.1 | 473  | 13 | BI778921 |
| 26 | 123.6 | 28.1 | 578  | 14 | BQ759854 |
| 27 | 123.6 | 28.1 | 601  | 14 | BQ767075 |
| 28 | 123.6 | 28.1 | 608  | 14 | BQ765728 |
| 29 | 123.6 | 28.1 | 621  | 13 | BM370509 |
| 30 | 123.6 | 28.1 | 636  | 12 | BF625593 |
| 31 | 123.6 | 28.1 | 650  | 13 | BI958490 |
| 32 | 123.6 | 28.1 | 655  | 13 | BI778583 |
| 33 | 123.6 | 28.1 | 800  | 12 | BE299552 |
| 34 | 123.6 | 28.1 | 865  | 12 | BF620735 |
| 35 | 123.6 | 28.1 | 879  | 13 | BI949512 |
| 36 | 123.4 | 28.0 | 992  | 10 | BE040565 |
| 37 | 123.2 | 28.0 | 411  | 9  | AL828336 |
| 38 | 123.2 | 28.0 | 539  | 9  | AL825800 |
| 39 | 123.2 | 28.0 | 554  | 12 | BE262856 |
| 40 | 122.6 | 27.9 | 668  | 9  | AL504667 |
| 41 | 122.4 | 27.8 | 399  | 14 | BQ606346 |
| 42 | 122.4 | 27.8 | 577  | 12 | BF474747 |
| 43 | 121.8 | 27.7 | 445  | 9  | AU172608 |
| 44 | 121.6 | 27.6 | 431  | 12 | BG314081 |
| 45 | 121.6 | 27.6 | 475  | 12 | BG312596 |

#### ALIGNMENTS

RESULT 1  
AY108359  
LOCUS AY108359 Zea mays PC0061446 mRNA sequence.  
DEFINITION Zea mays  
ACCESSION AY108359  
VERSION AY108359.1 GI:21211437  
KEYWORDS HTC.  
SOURCE Zea mays.  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,  
Arthur,L.W., Hanafey,M., Morgante,M. and finney,S.V.  
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of  
Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 974)  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,  
Arthur,L.W., Hanafey,M., Morgante,M. and finney,S.V.  
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of  
Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 974)  
AUTHORS Coe,E.C.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
Missouri, Columbia, MO 65211, USA  
FEATURES  
source  
1..974  
/organism="Zea mays"  
/db\_xref="MaizeDB:633254"  
/db\_xref="taxon:4577"  
/clone="PC0061446"

AY108359 974 bp mRNA linear HTC 25-MAY-2002

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/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration with the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT      235 a  234 c  257 g  248 t
ORIGIN

Query Match      60.8%; Score 267.6; DB 11; Length 974;
Best Local Similarity 78.0%; Pred. No. 4.7e-61;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 1 CGTCCGCGCGCGGACGCTTCCTTCCTCCCGCGGTCAGCGTCGCGGCTCCNNTGAGC 60
Db 26 CGTCCGCGCGCGGACGCGCCGCTTCCTCCCGCGGTCAGCGTCGCGGCTCCACTGAGC 85

Qy 61 GTGCGCGTCACCGCGGCGGAGCGGCGGTCGTCGCGGTCGCGGTCGTCGTCGTCG 120
Db 86 GTGCGGTGTACCGCGGCGGAGCGGCGGTCGTCGCGGTCGCGGTCGTCGTCGTCG 145

Qy 121 CGCTTGGCGGNGATCGNCTCTCNATCNGTATNCCCGACTTNCACAGCCAGGGATN 180
Db 146 CGCTTGGCGGNGATCGCTCTCCATCCGCTCATCCCGGCTTCCTCCCGAGCCAGGATC 205

Qy 181 ATGTTTCAGGACATCANGANGNTGTTTCATCCCAAGCGGTCCTGTCACACATATAC 240
Db 206 ATGTTTCAGGACATCAGACGCTGTCGTCGATCCCAAGCGGTCCTGTCGACCATGAC 265

Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACCCNTGGAAATAGGAGTTAAAGCTAG 300
Db 266 CTCCTTGTGCGAGCGGTACAAGGACCAAGGATACCCGTTGCT-GGTGTTGAAGCTAG 324

Qy 301 AGGNTCANTTTCCGAACAACATNTCTTANAANNAATTTGTCAAAAATNGTGNCAATT 360
Db 325 AGGTTTCATTTTGGTCTCTCTATCGCTT--TAGCCATTTGGCGCAAAATTTGTGCCT-TT 381

Qy 361 GAGGAAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATTTTNGGAATNN 420
Db 382 GAGNAGCGGAGAGGTTGCCAGGGAGGTGATCT--CCGAAGAGTATCTTTTGGAAATAT 439

Qy 421 GGAATNTAGATAAAAAAANT 440
Db 440 GGAAGTACAAGATAGAAAT 459

RESULT 2
AW424591      492 bp  mRNA  linear  EST 09-FEB-2000
LOCUS      707018G10.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea
DEFINITION  mays cDNA, mRNA sequence.
ACCESSION  AW424591
VERSION    AW424591.1 GI:6952523
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
            Walbot,V.
            Maize ESTs from various cDNA libraries sequenced at Stanford
            University
            Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
```

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Plate: 707018 row: G column: 10.
Location/Qualifiers
1. .492
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: tassel, kernel, silk, husk, root, leaf;
vector: pGAD10; Site:1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
BASE COUNT      89 a  146 c  149 g  106 t  2 others
ORIGIN

Query Match      60.6%; Score 266.6; DB 10; Length 492;
Best Local Similarity 78.0%; Pred. No. 6.8e-61;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 1 CGTCCGCGCGCGGACGCTTCGCTTCCTCCCGCGGTCAGCGTCGCGGCTCCNNTGAGC 60
Db 21 CGTCCGCGCGCGGACGCGCGCTTCCTCCCGCGGTCAGCGTCGCGGCTCCACTGAGC 80

Qy 61 GTGCGCGTCACCGCGGCGGAGCGGTCGTCGCGGTCGTCGTCGTCGTCGTCGTCG 120
Db 81 GTGCGGTGTACCGCGGCGGAGCGGCGGTCGTCGCGGTCGTCGTCGTCGTCGTCG 140

Qy 121 CGCTTGGCGGNGATCGNCTCTCNATCNGTATNCCCGACTTNCACAGCCAGGGATN 180
Db 141 CGCTTGGCGGNGATCGCTCTCTCATCCCGGTCATCCCGGCTTCCTCCAGCCAGGATC 200

Qy 181 ATGTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGGTCCTGTCACACATATAC 240
Db 201 ATGTTTCAGGACATCAGACGCTTGTCTGTCGATCCCAAGCGGTCCTGTCACACATC 260

Qy 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACCCNTGGAAATAGGAGTTAAAGCTAG 300
Db 261 CTCCTTGTGCGAGCGGTACAAGGACCAAGGATACCCGTTGCT-GGTGTTGAAGCTAG 319

Qy 301 AGGNTCANTTTCCGAACAACATNTCTTANAANNAATTTGGTCAAAAATNGTGNCAATT 360
Db 320 AGGTTTCATTTTGGTCTCTCTATCGCTT--TAGCCATTTGCGCAAAATTTGTGCCT-TT 376

Qy 361 GAGGAAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATTTTNGGAATNN 420
Db 377 GAGGAAGCCGAAGAAGNTGCCAGGCGAGGTGATCT--CCGAAGAGTATTTTGGAAATAT 434

Qy 421 GGAATNTAGATAAAAAAANT 440
Db 435 GGAAGTACAAGATAGAAAT 454

RESULT 3
BO487045      646 bp  mRNA  linear  EST 07-JUN-2002
LOCUS      1091050G11.y1 1091 - Immature ear with common ESTs screened by
DEFINITION  Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION  BO487045
VERSION    BO487045.1 GI:21331664
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
            Walbot,V.
            Maize ESTs from various cDNA libraries sequenced at Stanford
            University
```

JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1091050 row: G column: 11.  
Location/Qualifiers  
1. 646  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="1091 - Immature ear with common ESTs screened by Schmidt lab"  
/tissue\_type="Inflorescence meristem - floral organ  
Primordia"  
/dev\_stage="0.5 cm to 2 cm"  
/lab\_host="Stratagene XL0LR"  
/note="Organ: Immature ear; Vector: PAD-GAL4; Site\_1: EcoRI; Site\_2: XhoI; RNA from library 606 was filtered for common ESTs found in 606."  
BASE COUNT 130 a 165 c 198 g 153 t  
ORIGIN

Query Match 58.8%; Score 258.6; DB 14; Length 646;  
Best Local Similarity 77.5%; Pred. No. 1e-58;  
Matches 334; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 10 CGGCGCAGTTCGCCCTTTTCGTCGCCGCTCAGCGTGCAGGTCGCGGTCNNNTGAGCGTGGCGTC 69  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 1 CGGCGAGCCGCCCTTTTCGTCGCCGCTCAGCGTGCAGGTCGCGGTCGCCACTGAGCGTGGCGTC 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 70 ACCGGCGAGCGAGGCGAGCGCGTGTGGCGATGGCGTNGCGTATGCCGCTGGCGG 129  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 61 ACCGGGGAGGCAAGGCGAGCGGTGTGGCGATGGCGTCCGCTGCGCGCGCTGGCGG 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 130 GNGATCGNCTCTNCATCCNGGTATNCCGACTTNCAGAGCCAGGATNATGTTTCAG 189  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 121 GGGATCGCTCTCCATCCGCGTCTCCCGACTTCCCGAGCCAGGATCATGTTCCAG 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 190 GACATCANGANGNTGTTGATCCCAAGCGGNTCCGTGACACATATACATTTTGTG 249  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 181 GACATCAGACGTTGCTGCTGATCCCAAGCGGTTCCGTGACACCATCGACTCTTTGTC 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 250 AAGCGGTACAAGGACCAAGGNATCAACNTGGAANTAGGAGTTAAAGCTAGAGGNTCAN 309  
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Db 241 GAGCGGTACAAGGACCAAGGATCACCGTGGTGTGCT -GGTGTGAAGCTAGAGGTTTCAT 299  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 310 TTTTCGGAACAACATANNCTTTANAANNAATTTGTCAAAAATNGTGNCNATTTGAGGAACN 369  
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Db 300 TTTTGGTCTCTCTATCGCTT--TAGCCATTGGCGCAAAATTTGTCCTT-TTGAGGAAGCC 356  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 370 NAATWAGTGGCAGCNAAATGATTTTNGAATANGAATTTTNGGAATNNGAATNNTA 429  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 357 GAAGAAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTGGAATATGGAAGTAC 414  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 430 GATAAAAAAT 440  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 415 AAGATAGAAAT 425  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

RESULT 4  
AI948185  
LOCUS 491 bp mRNA linear EST 19-AUG-1999  
DEFINITION 603037E02.xl 603 - stressed root cDNA library from Wang/Bohnert lab  
Zea mays cDNA, mRNA sequence.  
ACCESSION AI948185  
VERSION AI948185  
KEYWORDS EST.  
SOURCE AI948185.1 GI:5740495  
ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS 1 (bases 1 to 491)  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 603037 row: E column: 02.  
Location/Qualifiers  
1. 491  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="603 - stressed root cDNA library from Wang/Bohnert lab"  
/tissue\_type="Seedling"  
/dev\_stage="salt stress"  
/lab\_host="E. coli XL Gold"  
/note="Organ: root; Vector: pBluescriptII SK(+); XR;  
Seedling stressed root cDNA library from Wang/Bohnert lab"  
BASE COUNT 76 a 165 c 148 g 100 t 2 others  
ORIGIN

Query Match 56.0%; Score 246.6; DB 9; Length 491;  
Best Local Similarity 83.6%; Pred. No. 1.5e-55;  
Matches 275; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 1 CGTCCGCGCGGCGACTTCGCTTTTCGTCGCCGCTCAGCGTCGCGGTCNNNTGAGC 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 163 CGTCCGCGCGGCGAGCGGCTTTTCGTCGCCGCGGAGCGTCGCGGCTCCACTGAGC 222  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 61 GTGGCGCTCACCGGCGGAGGCGAGCGGTCGTCGCGATGGCGTNGCGTATGTCG 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 223 GTGGCTGTACCGGCGGAGGCAAGGCGAGCGGTGTGGCGATGGCGTCCGCTGAGCG 282  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 121 CGTTGGCGNGATCGNCTCTNCATCCNGGTATNCCGACTTNCAGAGCCAGGATN 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 283 CGCTTGGCGGGATCGCTCTCCATCCGCTATCCCGACTTCCCGAAGCCAGGATC 342  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 181 ATGTTTCAGGACATCANGANGNTGTTGATCCCAAGCGGNTCCGTGACACATATAC 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 343 ATGTTCCAGGACATCAGGACGTTGCTGCTGATCCCAAGCGGTTCCGTGACACATCGAC 402  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 241 CATTTGTCAAGCGGTACAGGACCAAGGNATCAACNTGGAANTAGGAGTTAAAGCTAG 300  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 403 CTCCTTGTGAGCGGTACAGGACCAAGGATCACCGNGTGTGCT-GGTGTGAAGCTAG 461  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
QY 301 AGGNTCANTTTCCGAACAACACTANNCTTT 329  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
Db 462 AGGTTTCATTTTGGTCTCTCTATCGCTT 490  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

RESULT 5  
BE553166  
LOCUS 583 bp mRNA linear EST 10-AUG-2000  
DEFINITION 946089H09.yl 946 - tassal primordium prepared by Schmidt lab Zea  
mays cDNA, mRNA sequence.  
ACCESSION BE553166  
VERSION BE553166.1 GI:9794858  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 583)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
JOURNAL University  
COMMENT Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 946089 row: H column: 09.  
Location/Qualifiers  
1. 583  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassels primordium prepared by Schmidt lab"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to inflorescence development"  
/lab\_host="XLOLR"  
/note="Organ: tassels; Vector: HybridZAP; Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."  
BASE COUNT 114 a 157 c 175 g 137 t  
ORIGIN  
Query Match 51.2%; Score 225.2; DB 10; Length 583;  
Best Local Similarity 73.4%; Pred. No. 9e-50;  
Matches 309; Conservative 0; Mismatches 106; Indels 6; Gaps 4;  
Qy 20 CGCCTTTTCGTCGCCGCTCAGCGTCGCCGTCNNNTGAGCGTCGCCGTCACCGCGGCA 79  
Db 6 CGCCTTTTCGTCGCCGCTCAGCGTCGCCGTCNNNTGAGCGTCGCCGTCACCGCGGCA 65  
Qy 80 GCGAGGCGCGGTGTGCGATGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 139  
Db 66 GCGAGGCGCGGTGTGCGATGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 125  
Qy 140 CTCTCATCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGAT 199  
Db 126 CTCTCATCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGATCCCGCTGAT 185  
Qy 200 NGNTGNTGTCGATCCCGAGCGGNTGCGTGACACATATACATTTGTCAGCGGTACA 259  
Db 186 CACTGCTGTCGACCCCAAGCGGTTCGTCGACACCATCGACCTCTTCGTTGAGCGGTACA 245  
Qy 260 AGGACCAAGGATCACCTGGAANTAGGATTAAGCTAGAGGNTCANTTTCGGRACA 319  
Db 246 AGGACCAAGGATCACCTGGAANTAGGATTAAGCTAGAGGNTCANTTTCGGRACA 304  
Qy 320 ACTANNTCTTANAANAATTTGCTAAAAATNGGTGNCNATTTGAGGAACNNAAATNAGNTG 379  
Db 305 CCTATCGCT--CTAGCCATCGGTGCTAAATTTGT-ACCTTTGAGGAACCCGAAGAGTTG 361  
Qy 380 CCAGCNAATGATTTTNGAANTANGAATTTTNGGAATNNGAATNNTAGATAAAAAN 439  
Db 362 CCAGGCGAGGTGATCT--CCGAAGAATATTTCTGGAATACGGAACACTGACAGATAGAGA 419  
Qy 440 T 440  
Db 420 T 420  
RESULT 6  
B1233723 511 bp mRNA linear EST 11-JUL-2001  
LOCUS B1233723  
DEFINITION 949032B03.y2 949 - Juvenile leaf and shoot cDNA from Steve Moose

Zea mays cDNA, mRNA sequence.  
B1233723  
VERSION B1233723.1 GI:14701305  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 511)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949032 row: B column: 03.  
Location/Qualifiers  
1. 511  
/organism="Zea mays"  
/cultivar="W64A"  
/db\_xref="taxon:4577"  
/clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"  
/tissue\_type="immature leaf primordium and vegetative meristem"  
/dev\_stage="4 stages from 3-13 days after imbibing"  
/lab\_host="E. coli XLOLR"  
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site\_1: EcoRI; Site\_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda HybridZAP vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."  
BASE COUNT 105 a 130 c 156 g 120 t  
ORIGIN  
Query Match 50.6%; Score 222.8; DB 13; Length 511;  
Best Local Similarity 76.2%; Pred. No. 3.7e-49;  
Matches 308; Conservative 0; Mismatches 89; Indels 7; Gaps 5;  
Qy 37 GTCAGCGTCGCGCTCCNNTGAGCGTCGCGTCACCGCGGAGGAGGCGGCGGTG 96  
Db 1 GTCAGCGTCGCGCTCCACCTG-CGCTGCGTGTACCGCGGAGGAGGAGGCGGTTG 59  
Qy 97 GTGCGGATGCGGTGCGGTGATGCGGCTTGCGGNGATCGNCTCCTNCAATCCNGGTNATN 156  
Db 60 GTGCGGATGCGGTGCGGTGATGCGGCTTGCGGNGATCGCCTCCATCCGCGTCATC 119  
Qy 157 CCCGACTTNCAGGCGGATNATGTTTCAGGACATCANGANGTNGTGTTCGATCCC 216  
Db 120 CCCGACTTNCAGGCGGATNATGTTTCAGGACATCAGGAGTGTGCTGCTCGATCCC 179  
Qy 217 AAGCGGTCGTCGACATATACCATTTGTCAAGCGGTACAAGGACCAAGGNATCAC 276  
Db 180 AAGCGGTCGTCGACATCAGCATCGACCTCTTGTGCGAGGTCACAGGACCAAGGATCAC 239  
Qy 277 NTGGAANTAGGAGTTAAAGCTAGAGGNTCANTTTCGGAACAACACTANNTCTTANAANA 336  
Db 240 GTGGTTGCT-GGTGTTGACGTAGAGGTTTCATTTTGGTCTCCTATCGCTT--TAGCC 296

```
QY 337 ATTGTCATAAATNGTGNCAATTTGAGGAAGCANNAAATNAGNTGGCANGCNAATGATTTT 396
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 ATTGCGCAAAATTTGTCCT-TTGAGGAAGCGGAAGATTTGCCAGCGAGGTGATCT- 354

QY 397 NANGAATANGAATTTTNGAATNNGAATNTAGATAAAAAAANT 440
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 -CCGAAGAGTATTTCTTGGAAATGATGAAGAACTGACAAGATAGAAAT 397

RESULT 7
AW925193 531 bp mRNA linear EST 19-JUL-2000
LOCUS WSI_76_E10.bl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
DEFINITION mRNA sequence.
ACCESSION AW925193
VERSION AW925193.1 GI:8091019
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 531)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: water-stressed plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 458
POLYA-No.
FEATURES
source
1..531
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT 107 a 156 c 164 g 104 t
ORIGIN
Query Match 49.5%; Score 218; DB 10; Length 531;
Best Local Similarity 74.1%; Pred. No. 7.3e-48;
Matches 326; Conservative 0; Mismatches 102; Indels 12; Gaps 6;

QY 4 CCGCGCGCGCGGACATTCGCTTTTCGTCGCCGCTCAGCGTCGCGGCCTCCNNTGAGCGTG 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 93 CCGCGCGGCTGCGCGCGCGCTTTTCGTCGCCGCTCAGCGTCGCGGCCTCCGCTGAGCGTG 149
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 64 CGCGTCACCGCGCGGAGCGAG--GGCAGGCGGTGGTGGCGATGGCTNCGCTGATGCG 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 CGCGTCACCGCGGAGCGAGGAGCGAGCGGTGGTGGCGATGGCTCCGCACACGCG 209
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 CGCTTGGGNGATCGNCTCTNCAATCNGTNATNCCGACTTNCCAAAGCCAGGGATN 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 CGCTTGGGCGGATCGCTCTCCATCCGCTATCCCGACTTCCCAAGCCAGGGATC 269
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 ATGTTTCAGGACATCANGANGTNGTTCGATCCCAAGCGGNTCCGCACACATATAC 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 270 ATGTTCCAGGACATCAGACGTTGCTGCTCGACCCCAAGCGGCTTCCGTGACACCATGAC 329
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 241 CATTTTGTCAAGCGGTACAAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAAAGCTAG 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 330 CTCTTTTCTGAGCGCTCAAGGACCAAGGATCACCGTAGTTGCT-GGTGTTGAAGCTAG 388

QY 301 AGGNTCANTTTTCGGAACAACACTANNCTTTANAANNATTTGGTCAAAAATNGGTGNCNATT 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 389 AGGTTTCATTTTCGGTCTCTCTATCGCTT--TAGCCATCGGTGCAAAATTTGTGCCT-TT 445
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 361 GAGGAAGCNAATNAGNTGCCANGCNAATGATTTTNNANGAATANGAATTTTNGGAATNN 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 446 GAGAAAGCCAAAGAGTTGCCAGCGGAGTGATCT--CCGAAGAGTATCTTTTGGGAATAC 503

QY 421 GGAATNNTAGATAAAAAAANT 440
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 504 GGAAGTGAACAAGATCGAAAT 523
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
BE552951 508 bp mRNA linear EST 10-AUG-2000
LOCUS 946087G06.y1 946 - tassal primordium prepared by Schmidt lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION BE552951
VERSION BE552951.1 GI:9794643
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 508)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946087 row: G column: 06.
Location/Qualifiers
1..508
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/note="Organ: tassels; Vector: HybridZAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridZAP. Sample insert size range was 350 bp
to 3 kb with a 1 Kb average."
BASE COUNT 98 a 143 c 149 g 118 t
ORIGIN
Query Match 49.4%; Score 217.4; DB 10; Length 508;
Best Local Similarity 72.5%; Pred. No. 1e-47;
Matches 303; Conservative 0; Mismatches 109; Indels 6; Gaps 4;

QY 23 CTTTTCTCCCGGTACGCGTCAGCGTCCGCGTCCNNTGAGCGTGCGCGTACCAGCGGAGCG 82
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 CTTTTCGTCCCGGTCCGCGTCCGCGTCCACTCCACTGGCGTGCGCGTACCAGCGGAGCG 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 83 GAGGCGAGCGCGTGGTGGCGATGGCGTNGCGTGTATGCGCGCTTGGCGGNGATCGNCTCCT 142
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 GAGGCGAGCGCGTGGTGGCGATGGCGTCCGCGGACGCTCGTGGCGGGAATTGCTCCT 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



Matches 197; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 5 CGCGCGCGCGACTTTCGCTTTCGCTCCCGGTCAGCGTCGCGCTCCNNNTGAGCGTGC 64

Db 1 CGTCCGCTCCCGCGCGCTTTCGCTCCCGGTCGCGCTCCCGCTCCACTGGCGTGC 60

QY 65 GCGTCACCGCGCGGAGGCGAGGCGGCTGCGGTCGCGCTCCCGCTCCCGCTCCCGCT 124

Db 61 GCGTCACCGCGCGGAGGCGAGGCGGCTGCGGTCGCGCTCCCGCTCCCGCTCCCGCT 120

QY 125 TGCGGNGATGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 183

Db 121 TGCGGNGATGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 180

QY 184 TTTCAGGACATCANGANGNTGTTTCAGGACATCANGANGNTGTTTCAGGACATCANGANG 243

Db 181 TTTCAGGACATCANGANGNTGTTTCAGGACATCANGANGNTGTTTCAGGACATCANGANG 240

QY 244 TT 245

Db 241 TT 242

RESULT 11  
AL822592 450 bp mRNA linear EST 15-JUL-2002  
LOCUS

DEFINITION  
AL822592 p:335 Triticum aestivum cDNA clone E04\_p335\_plate\_10, mRNA  
sequence.

ACCESSION  
AL822592  
VERSION  
AL822592.1 GI:21834361  
KEYWORDS  
EST.  
SOURCE  
bread wheat.  
ORGANISM  
Triticum aestivum

REFERENCE  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
1 (bases 1 to 450)

AUTHORS  
Wilson, I., Beswick, R., Shepherd, S., Barker, G., Parker, J., Owen, P.,  
Edwards, D., Coghill, J., Holdsworth, M., Lenton, J., Shewry, P. and  
Edwards, K.

TITLE  
A BSRG-funded wheat EST resource for the academic community  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Barker G  
Institute of Arable Crop Research  
Long Ashton, Bristol BS41 9AF United Kingdom.

FEATURES  
Location/Qualifiers  
1..450  
/organism="Triticum aestivum"  
/cultivar="mercia"  
/db\_xref="taxon:4565"  
/clone="E04\_p335\_plate\_10"  
/tissue\_type="p:335"  
/dev\_stage="21 days old"  
/dev\_stage="21 days old"

BASE COUNT 88 a 137 c 131 g 94 t

ORIGIN

Query Match 28.9%; Score 127.2; DB 9; Length 450;  
Best Local Similarity 63.6%; Pred. No. 1.5e-23;  
Matches 227; Conservative 0; Mismatches 123; Indels 7; Gaps 4;

QY 39 CAGCGTCGCGGCTCCNNNTGAGCGTCCCGGTCAGCGTCCCGGTCAGCGTCCCGGTCAGCG 98

Db 73 CTGCGGTTCCGATCCCGCGGAGGCTGCGGCTCCCGGTCAGCGTCCCGGTCAGCGTCCCGG 132

QY 99 GCGGATGGGTCGCTGATGCGGCTTGGCGGNGATCGCTTCCTTCATCCGNGTATCC 158

Db 133 CCGGATGGGATCC--GAGCGGCGGTCGAGCGGATCGCGTCCAGCATCCCGCGCATCCC 189

QY 159 CGATTTCCAAAGCCAGGATGATGTTTCAGGACATCANGANGNTGTTTCAGGATCCCAA 218

Db 190 CAATTTCCCAAGCAGGATGATGTTTCAGGACATCACAACCTGCTCTCTCATCCGCA 249

QY 219 GCGNTCCGTGACACATATATACCATTTTGTCAAGCGGTACAAAGCAACCAAGNATCAC 278

Db 250 GGCATTCCTGACACCATGACCTCTTTGTGCGAGCGGTACAAAGCAACCAAGNATCAC 309

QY 279 GGAANTAGAGCTTAAGCTAGAGGNTCANTTTCGGAACAACATANNCTTTANANNAAT 338

Db 310 AGTTACT-GGTGTTGAAGCCAGAGGATTCATTTTGGTCTCCCATTCG--ATTAGCAT 366

QY 339 TGGTCAAAATNGTGTGNCNATTTAGGAAAGCNAATNAGTGTCCGANGNAAATGATTT 395

Db 367 AGGTGCAAAATTTGT-TCCAATAAGGAAGCCGAATAAATTAACCTGCTGAGGTGATAT 422

RESULT 12  
BH217843 453 bp DNA linear GSS 08-NOV-2001  
LOCUS

DEFINITION  
1005060C11.y1 1006 - RescueMu Grid G Zea mays genomic, DNA  
sequence.

ACCESSION  
BH217843  
VERSION  
BH217843.1 GI:16809899  
KEYWORDS  
GSS.  
SOURCE  
Zea mays.  
ORGANISM  
Zea mays

REFERENCE  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS  
Walbot, V.  
TITLE  
Maize genomic sequences found using engineered RescueMu transposon  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
plate: 1006060 row: 8  
Class: transposon-tagged.

FEATURES  
Location/Qualifiers  
1..453  
/organism="Zea mays"  
/cultivar="mixed background W23/AL88/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - RescueMu Grid G"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"

/note="Organ: leaf; Vector: RescueMu (engineered from  
pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
RescueMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescueMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

BASE COUNT 58 a 150 c 133 g 112 t

ORIGIN

Query Match 28.8%; Score 126.6; DB 17; Length 453;  
Best Local Similarity 82.6%; Pred. No. 2.1e-23;  
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 10 CGCGCCGACTTCGCTTTTCGTCGCCGCTCAGCGTCCGCGCTCCNNNTGAGCGTCCGCTC 69

Db 40 CGTCGCGCGCGCTTCTCTCGTCCCGCGTCGCGCTCCCGCTCCCGCTCCCGCTCCCGCTC 99

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QY 70 ACCGGCGCAGCGGAGCGGCTGCTGCGATGCGTNCGCTGATGCGCGCTTGGCG 129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 ACCGGCGGAGCGGAGCGGCTGCTGCGATGCGCTCCGCGACGCGCTTGGCG 159
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 GNGATCGCTCCTNATCCNGGNGTATNCCGAGCTTCCAAAGCCAGG 176
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 GGGATTGCTCTCCATCCGCGCTCATCCCGGACTTTCCTCCAAAGCCAGG 206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
LOCUS BE404891 603 bp mRNA linear EST 21-JUL-2000
DEFINITION WHE1206_D01_G02ZS Wheat etiolated seedling root cDNA library
            Triticum aestivum cDNA clone WHE1206_D01_G02, mRNA sequence.
ACCESSION BE404891
VERSION BE404891.1 GI:9364359
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
            1 (bases 1 to 603)
AUTHORS P.S., Hala, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Han
        Seaton, C.L. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat
        genomes
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
        US Department of Agriculture, Agriculture Research Service, Pacific
        West Area, Western Regional Research Center
        800 Buchanan Street, Albany, CA 94710, USA
        Tel: 5105595773
        Fax: 5105595818
        Email: oanderson@pw.usda.gov
        Sequences have been trimmed to remove vector sequence and low
        quality sequence with phred score less than 20
        Seq primer: Strategene SK primer.
FEATURES             Location/Qualifiers
     source           1..603
                    /organism="Triticum aestivum"
                    /cultivar="Chinese Spring"
                    /db_xref="taxon:4565"
                    /clone_lib="WHE1206_D01_G02"
                    /clone_lib="Wheat etiolated seedling root cDNA library"
                    /tissue_type="Root"
                    /dev_stage="Five day old etiolated seedling"
                    /lab_host="E. coli SOLR"
                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                    Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
                    , germinated and grown aseptically in the dark at room
                    temperature on filter paper with water, nystatin and
                    cefotaxime in covered crystallization dishes. Roots were
                    harvested. The tissue, total RNA, and poly(A) RNA were
                    prepared, a cDNA library was made, and the cDNA clones
                    were in vivo excised to give pBluescript phagemids in the
                    TJ Close lab (Choi, Close, Fenton) at the University of
                    California, Riverside. Plasmid DNA preparations and DNA
                    sequencing were performed in the OD Anderson lab (all
                    other authors)."
     BASE COUNT      131 a 153 c 182 g 137 t
     ORIGIN

Query Match      28.7%; Score 126.4; DB 10; Length 603;
Best Local Similarity 55.3%; Pred. No. 2.7e-23;
Matches 233; Conservative 0; Mismatches 116; Indels 8; Gaps 5;

QY 39 CAGCGTCGCGCTCCNNTGATCGCTGCTACGCGCGGAGCGGAGCGGCGTGGT 98
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 CTGCGGTTCCGATCCCCCGGAGGCGTGCCTGCGC-GCGGCGAGGGTTCGCGCGCT 89
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 99 GCGATGCGCTNCGCTGATCGCGCTTGGCGGNGATCGCTCTNCAATCNGGNTATNCC 158
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 90 CGCATGCGATCC--GACGGGCGTGGAGCGATCGCTCCAGCATCGGCGCCATCCC 146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 159 CGACTTNCACAGCCAGGATNATGTTTCAGGACATCANGANGTNTGTTCCGATCCCAA 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 CAATCTCCCAAGCCAGGATTTGTTTCAGGACATCAACAACCTTCTCTCGATCCGCA 206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 219 GCGGTCGCTGACACATATACCATTTTGTCAAGCGGTACAAAGGACCAAGGATACCTT 278
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 GGCATTCGCTGACACCACTGACCTCTTTGTCGAGCGGTACAAAGGACATCACTCT 266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 279 GGAAATAGGAGTTAAAGCTAGAGGNTCANTTTCCGAACAACCTANTTCTANNAAT 338
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 AGTTGCTTGGTGTGAAGCCAGAGGATTCATTTTGGTCTCTCCCATGTC--ATTAGCCAT 323
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 339 TGGTCAAAATNGGTGNCNATTTGAGGAAGCNAATNAGTNGCCANGCNAATGATTT 395
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 AGGTGCAAAAGTTTGT-TCCAATAGGAAGCCAAAATAATTACCTGGTGGTGATAT 379
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
LOCUS BQ483893 791 bp mRNA linear EST 03-JUN-2002
DEFINITION WHE3513_G10_M19ZS Wheat unstressed root cDNA library Triticum
            aestivum cDNA clone WHE3513_G10_M19, mRNA sequence.
ACCESSION BQ483893
VERSION BQ483893.1 GI:21319829
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
            1 (bases 1 to 791)
AUTHORS Anderson, O.D., Chao, S., Close, T.J., Crossman, C., Fenton, R.D., Lazo
        G.R., Nguyen, H.T., Rausch, C.J., Wilson, C., Woo, J. and Zhang, D.
TITLE The structure and function of the expressed portion of the wheat
        genomes - Unstressed root cDNA library
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
        US Department of Agriculture, Agriculture Research Service, Pacific
        West Area, Western Regional Research Center
        800 Buchanan Street, Albany, CA 94710, USA
        Tel: 5105595773
        Fax: 5105595818
        Email: oanderson@pw.usda.gov
        Sequences have been trimmed to remove vector sequence and low
        quality sequence with phred score less than 20
        Seq primer: SK primer.
FEATURES             Location/Qualifiers
     source           1..791
                    /organism="Triticum aestivum"
                    /cultivar="Chinese Spring"
                    /db_xref="taxon:4565"
                    /clone_lib="WHE3513_G10_M19"
                    /clone_lib="Wheat unstressed root cDNA library"
                    /tissue_type="Roots"
                    /dev_stage="Full tillering"
                    /lab_host="E. coli SOLR"
                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                    pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants
                    were grown until full tillering stage and root tissue was
                    collected at Texas Tech University (Zhang, HT Nguyen Lab
                    ). Total RNA and poly(A) RNA were prepared, a cDNA
                    library was made, and the cDNA clones were in vivo
                    excised to give pBluescript SK(-) phagemids in the TJ
                    Close lab (Close, Fenton) at the University of California
                    , Riverside. Colony plating, plasmid DNA preparations
                    and DNA sequencing were performed in the OD Anderson lab
                    (all other authors)."
     BASE COUNT      171 a 215 c 222 g 183 t
     ORIGIN

```



Query Match 28.7%; Score 126.4; DB 14; Length 791;  
 Best Local Similarity 65.3%; Pred. No. 3e-23;  
 Matches 233; Conservative 0; Mismatches 116; Indels 8; Gaps 5;

QY 39 CAGCGTCGGCGTCCNNNTGAGCGTCCGGTCCAGCGCGGAGGCGGCGGTGGT 98  
 DB 104 CTGCGGTTCCGATCCCGCGGAGCGTCCGGTTCGGC-GCGGGGAGGCGTGGCGGCGGT 162

QY 99 GCGCGATGGCTNCGCTGATGGCGCGTTCGGCGNGATCGNCTCCCTNCATCCNNGGTNATNCC 158  
 DB 163 CGCGATGGCATCC---GACGGGCGGTGGAGCGGATCCGTCAGCATCCCGCCATCC 219

QY 159 CGAGTNNCCAAAGCAGGATNATGTTTCAGGACATCANGANGTNGTTCGATCCCAA 218  
 DB 220 CAACATCCCAAGCAGGATTTGTTTCAGGACATCAACACCTTGCTTCGATCCGCA 279

QY 219 GCGGNTCCGTGACACATATACATTTTGTCAAGCGGTACAGGACCAAGGATNATCAACNT 278  
 DB 280 GCGATCCGTGACACACTGACCTCTTTGTCGAGCGGTACAGGACCAAGACATCACTGT 339

QY 279 GGAANTAGGAGTTAAAGTAGAGGNTCANNTTCGGAACAACTANNVCTTANANNAAT 338  
 DB 340 AGTTCGT-GGTGTTGAAGCAGGATTCATTTTGGTCTCCCATTCG--ATTAGCCAT 396

QY 339 TGGTCAAAAATNGGTGNCNATTTGAGCAAGCNAATNAGTTCGCAAGCNAATGATTT 395  
 DB 397 AGGTGCAAGTTGT-TCCAATAAGGAAGCCCAAAAATTTACCTGGTGAGGTGATAT 452

RESULT 15  
 BE421015  
 LOCUS  
 DEFINITION HWM004.H08 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone  
 HWM004.H08, mRNA sequence.

ACCESSION BE421015  
 VERSION BE421015.1 GI:9418858

KEYWORDS EST.

SOURCE Hordeum vulgare.

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 : Triticeae; Hordeum.

REFERENCE

AUTHORS

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier  
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,  
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,  
 Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,  
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
 Sorrells, M., Warburton, M. and Wenzel, G.

International Triticeae EST Cooperative (ITEC); Production of

Expressed Sequence Tags for Species of the Triticeae

Unpublished (2000)

Contact: Herrmann RG

Botanisches Institut der LMU

Menzinger Str. 67, D-80638 München GERMANY

Fax: 49 30 171683

Email: herrmann@botanik.biologie.uni-muenchen.de

International Triticeae EST Cooperative (ITEC)

http://wheat.pw.usda.gov/genome.

Location/Qualifiers

FEATURES

source

1..1206

/organism="Hordeum vulgare"

/cultivar="Barke"

/db\_xref="taxon:4513"

/clone="HWM004.H08"

/clone\_lib="ITEC HWM Barley Leaf Library"

/tissue\_type="leaf"

/dev\_stage="14 day old"

/note="Vector: pBluescriptSK(-); 850 bp average insert

size."

BASE COUNT

ORIGIN

294 a 257 c 375 g 280 t

Query Match 28.4%; Score 125; DB 10; Length 1206;  
 Best Local Similarity 64.3%; Pred. No. 8.4e-23;  
 Matches 207; Conservative 0; Mismatches 108; Indels 7; Gaps 3;

QY 74 CCGGCAAGCGAGCGCGGTGGTGGCGATGGCGTNCCTGATGCGCGCTTGGCGGNGA 133  
 DB 43 GAGGCGGCGAGGGTCCGGCGGCTCGCGATGGCATCC---GACGGGCGGTGGAGCGGA 99

QY 134 TCGNCTCCTNCATCCNNGGTNATNCCGACTTNCCAAAGCCAGGATNATGTTTCAGGACA 193  
 DB 100 TCGGCTCCAGCATCCGCGCATCCCAACTTCCCAAGCCAGGATTTGTTTTCAGGACA 159

QY 194 TCANGANGTNGTNGTTCGATCCCAAGCGGNTCCGTCGACAAATATACATTTTGTCAAGC 253  
 DB 160 TCACAACCTTGTCTTCGATCCAGGCAATCCCGTGACACACAGACCTCTTTTGTGAGC 219

QY 254 GGTACAAGGACCAAGGNATCACCNNTGGAAANTAGGAGTTAAAGCTAGAGGNTCANTTTC 313  
 DB 220 GGTACAAGGACCAAGGACATACTGTAGTTGCT-GGTGTTGAAGCCAGAGGATTCATTTT 278

QY 314 GGAACAACCTANNVCTTANANNAATTTGGTCAAAAATNGTGNCHNATTCAGGAAGCNAAT 373  
 DB 279 GGGCCCCCTTATTCGATTTAGCCATAGGTGCGAAGTTTG---TTCCAATAAGGAAGCCGAAA 335

QY 374 NAGNTGCCANGCNAATGATTT 395  
 DB 336 AAACCTACCTGGTGAGGTGATAT 357

Search completed: November 30, 2002, 06:27:36  
 Job time : 2093 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 04:02:32 ; Search time 3363 Seconds  
(without alignments)  
3289.532 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtccgcgcgcgcgcacttc.....ggaatnntagataaaaaant 440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 24791104 seqs, 12571243825 residues  
Total number of hits satisfying chosen parameters: 495822208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main :\*

1: /cgn2\_6/ptodata/1/pna/pctus\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*  
14: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*  
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19: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*  
21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*  
22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*  
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25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
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29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*  
36: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*  
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41: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | Description           |
|------------|-------|---------------|--------|----|-----------------------|
| 1          | 396   | 90.0          | 440    | 16 | US-09-227-586-5       |
| 2          | 396   | 90.0          | 440    | 36 | US-09-976-054-5       |
| 3          | 275.6 | 62.6          | 566    | 33 | US-09-865-439A-110502 |
| 4          | 275.6 | 62.6          | 586    | 33 | US-09-865-419A-34849  |
| 5          | 275.6 | 62.6          | 586    | 64 | US-60-208-063-17908   |
| 6          | 275.6 | 62.6          | 593    | 33 | US-09-865-419A-40126  |
| 7          | 275.6 | 62.6          | 593    | 64 | US-60-208-063-23182   |
| 8          | 275.6 | 62.6          | 892    | 42 | US-10-219-999-25058   |
| 9          | 267.6 | 60.8          | 626    | 33 | US-09-865-439A-27582  |
| 10         | 267.6 | 60.8          | 626    | 64 | US-60-207-458-71879   |
| 11         | 267.6 | 60.8          | 640    | 27 | US-09-696-664A-10668  |
| 12         | 267.6 | 60.8          | 961    | 42 | US-10-219-999-7177    |
| 13         | 267.6 | 60.8          | 961    | 75 | US-60-312-544-3121    |
| 14         | 265.8 | 60.4          | 462    | 19 | US-09-513-996A-69703  |
| 15         | 264.4 | 60.1          | 572    | 33 | US-09-865-439A-82458  |
| 16         | 264.4 | 60.1          | 572    | 64 | US-60-207-458-126600  |
| 17         | 264.4 | 60.1          | 961    | 25 | US-09-654-617-266001  |
| 18         | 264.4 | 60.1          | 961    | 27 | US-09-684-016-266001  |
| 19         | 262.8 | 59.7          | 431    | 16 | US-09-227-586-27      |
| 20         | 262.8 | 59.7          | 431    | 36 | US-09-976-054-27      |
| 21         | 254.8 | 57.9          | 591    | 27 | US-09-696-664A-11136  |



|   |                           |               |  |
|---|---------------------------|---------------|--|
| ; | PRIOR FILING DATE:        | 1998-05-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/086,185 |  |
| ; | PRIOR FILING DATE:        | 1998-05-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/086,184 |  |
| ; | PRIOR FILING DATE:        | 1998-05-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/086,188 |  |
| ; | PRIOR FILING DATE:        | 1998-05-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/089,524 |  |
| ; | PRIOR FILING DATE:        | 1998-06-16    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/089,810 |  |
| ; | PRIOR FILING DATE:        | 1998-06-18    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/089,814 |  |
| ; | PRIOR FILING DATE:        | 1998-06-18    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/090,170 |  |
| ; | PRIOR FILING DATE:        | 1998-06-22    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/092,036 |  |
| ; | PRIOR FILING DATE:        | 1998-07-08    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/099,670 |  |
| ; | PRIOR FILING DATE:        | 1998-09-09    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/099,697 |  |
| ; | PRIOR FILING DATE:        | 1998-09-09    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/100,674 |  |
| ; | PRIOR FILING DATE:        | 1998-09-16    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/101,132 |  |
| ; | PRIOR FILING DATE:        | 1998-09-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/101,130 |  |
| ; | PRIOR FILING DATE:        | 1998-09-21    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/101,508 |  |
| ; | PRIOR FILING DATE:        | 1998-09-22    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/101,344 |  |
| ; | PRIOR FILING DATE:        | 1998-09-22    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/101,347 |  |
| ; | PRIOR FILING DATE:        | 1998-09-22    |  |
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| ; | PRIOR FILING DATE:        | 1998-09-22    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/104,126 |  |
| ; | PRIOR FILING DATE:        | 1998-10-13    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/104,127 |  |
| ; | PRIOR FILING DATE:        | 1998-10-13    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/104,124 |  |
| ; | PRIOR FILING DATE:        | 1998-10-13    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/104,121 |  |
| ; | PRIOR FILING DATE:        | 1998-10-13    |  |
| ; | PRIOR APPLICATION NUMBER: | US 60/111,981 |  |
| ; | PRIOR FILING DATE:        | 1998-12-11    |  |
| ; | PRIOR APPLICATION NUMBER: | US 09/199,129 |  |
| ; | PRIOR FILING DATE:        | 1998-11-24    |  |
| ; | PRIOR APPLICATION NUMBER: | US 09/210,297 |  |
| ; | PRIOR FILING DATE:        | 1998-12-08    |  |
| ; | PRIOR APPLICATION NUMBER: | US 09/227,586 |  |
| ; | PRIOR FILING DATE:        | 1999-01-08    |  |
| ; | NUMBER OF SEQ ID NOS:     | 711           |  |

| Query Match           | 90.0%        | Score 336;         | DB 36;        |
|-----------------------|--------------|--------------------|---------------|
| Best Local Similarity | 100.0%;      | Pred. No. 1.2e-99; | Length 440;   |
| Matches 440;          | Conservative | 0;                 | Mismatches 0; |
|                       |              |                    | Indels 0;     |
|                       |              |                    | Gaps 0;       |

|  | Qy | 121 | CGCTTGGCGNGATCGNCTCCTTNCATCCNGGTTNATNCCCAGACTTTC  | 181 | NCCAAAGCCAGGGATN |
|--|----|-----|---|-----|------------------|
|  | Qy | 121 | CGCTTGGCGNGATCGNCTCCTTNCATCCNGGTTNATNCCCAGACTTTC <td>181</td> <td>NCCAAAGCCAGGGATN</td> | 181 | NCCAAAGCCAGGGATN |
|  | Qy | 181 | ATGTTTCCAGGACATCANGANGNTGNTCTTCGATCCCAAGCGGNTCCGTGACACATATAC                            | 240 | TATAC            |
|  | Qy | 181 | ATGTTTCCAGGACATCANGANGNTGNTCTTCGATCCCAAGCGGNTCCGTGACACATATAC                            | 240 | TATAC            |
|  | Qy | 241 | CATTTTGTCAAGCGGTACAAAGGACCAAGGNATCACCNCTGGAAATAGGAGT                                    | 300 | TAAAGCTAG        |
|  | Qy | 241 | CATTTTGTCAAGCGGTACAAAGGACCAAGGNATCACCNCTGGAAATAGGAGT                                    | 300 | TAAAGCTAG        |
|  | Qy | 301 | AGGNTCANITTCGGAACAACACTANNTCTTANAANNAATTCGTCAAAAATNGGTGNCNATT                           | 360 | TTT              |
|  | Qy | 301 | AGGNTCANITTCGGAACAACACTANNTCTTANAANNAATTCGTCAAAAATNGGTGNCNATT                           | 360 | TTT              |
|  | Qy | 361 | GAGGAAGCNNAATNAGNTGCCANGCNAAAATGATTTTANGAATANGAATTTTNGGAATNN                            | 420 | TNN              |
|  | Qy | 361 | GAGGAAGCNNAATNAGNTGCCANGCNAAAATGATTTTANGAATANGAATTTTNGGAATNN                            | 420 | TNN              |
|  | Qy | 421 | GGAAATNTAGATAAAAAAAT 440  |     |                  |
|  | Qy | 421 | GGAAATNTAGATAAAAAAAT 440  |     |                  |

RESULT 3

US-09-865-439A-110502

; Sequence 110502, Application US/09865439A

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; APPLICANT: Hardeman, Kristine J.

; APPLICANT: La Rosa, Thomas J.

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(51936)B

; CURRENT APPLICATION NUMBER: US/09/865,439A

; CURRENT FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: US 60/207,458

; PRIOR FILING DATE: 2000-05-30

; NUMBER OF SEQ ID NOS: 119125

; SEQ ID NO 110502

; LENGTH: 566

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(566)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: LIB3732-014-Q1-K6-C3

US-09-865-439A-110502

|                       |              |                    |                |             |
|-----------------------|--------------|--------------------|----------------|-------------|
| Query Match           | 62.6%        | Score 275.6;       | DB 33;         | Length 566; |
| Best Local Similarity | 79.1%        | Pred. NO. 5.le-66; |                |             |
| Matches 348;          | Conservative | 0;                 | Mismatches 86; | Indels 6;   |
| Gaps                  |              |                    |                |             |

Query Match 90.0%; Score 396; DB 36; Length 440;  
Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps

Db 268 CTCTTTGTCGAGCGGTACAAGGACCAAGGATCACCGTGTGCT-GGTGTGAAGCTAG 326  
Qy 301 AGGNTGTCATTTTCGGAACAACATNTCTTANAANNAATTTGGTCAAAAATGGTGCNATTT 360  
Db 327 AGGTTTCATTTTCGGTCTCTATCGCTT--TAGCCATCGCGCAAAAATTTGTGCCT-TT 383  
Qy 361 GAGGAAGCNAATNAGNTGCCANGCNAATAATGATTTTANGAATANGAATTTTNGGAATNN 420  
Db 384 GAGGAAGCGGAAGAAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTTGAATAT 441  
Qy 421 GGAATNTAGATAAAAAANT 440  
Db 442 GGAAGTGAAGAATAGATAAT 461

RESULT 4  
US-09-865-419A-34849  
; Sequence 34849, Application US/09865419A  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51935)B  
; CURRENT APPLICATION NUMBER: US/09/865,419A  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/208,063  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 54020  
; SEQ ID NO 34849  
; LENGTH: 586  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(586)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3600-035-Q6-K6-E7  
US-09-865-419A-34849

Query Match 62.68; Score 275.6; DB 33; Length 586;  
Best Local Similarity 79.18; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;  
Qy 1 CGTCCGCGCGCGGACTTCGCCCTTTTCGTCGCCGCGGTACGCGTCCGCGGTCCNNTGAGC 60  
Db 63 CGTCCGCGCGCGGACGCGCGCTTTTCGTCGCCGCGGTACGCGTCCGCGGTCCACTGAGC 122  
Qy 61 GTGCGGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGGCGTGCCTGATGCG 120  
Db 123 GTGCGGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGGCGTCCGCTGATGCG 182  
Qy 121 CGCTTGGCGGNGATCGNCTCTTCATCCGCTNATCCCGACTTNCCTCAAGCCAGGATN 180  
Db 183 CGCTTGGCGGNGATCGCTCTCCATCCGCGTATCCCGACTTCCCAAGCCAGGATC 242  
Qy 181 ATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGNTCCGTGACACATATAC 240  
Db 243 ATGTTTCAGGACATCAGACGCTTGTCTCGATCCCAAGCGTCCGTGACACCATCGAC 302  
Qy 241 CATTTTGTCAAGCGGTACAGGACCAAGGNATCACCNWGGAAANTAGGATTAAGCTAG 300  
Db 303 CTCTTTGTCGAGCGGTACAAGGACCAAGGATCACCGTGTGCT--GGTGTGAAGCTAG 361  
Qy 301 AGGNTGTCATTTTCGGAACAACATNTCTTANAANNAATTTGGTCAAAAATGGTGCNATTT 360  
Db 362 AGGTTTCATTTTCGGTCTCTATCGCTT--TAGCCATCGCGCAAAAATTTGTGCCT-TT 418  
Qy 361 GAGGAAGCNAATNAGNTGCCANGCNAATAATGATTTTANGAATANGAATTTTNGGAATNN 420  
Db 419 GAGGAAGCGGAAGAAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTTGAATAT 476

Qy 421 GGAATNTAGATAAAAAANT 440  
Db 477 GGAAGTGAAGAATAGATAAT 496  
RESULT 5  
US-60-208-063-17908  
; Sequence 17908, Application US/60208063  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Laigudi, Raghunath V.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Shukla, Hridayabhiranjan  
; APPLICANT: Wu, Kunsheng  
; APPLICANT: Xu, Nanfei  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51935)A  
; CURRENT APPLICATION NUMBER: US/60/208,063  
; CURRENT FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 25021  
; SEQ ID NO 17908  
; LENGTH: 586  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3600-035-Q6-K6-E7  
US-60-208-063-17908  
Query Match 62.68; Score 275.6; DB 64; Length 586;  
Best Local Similarity 79.18; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;  
Qy 1 CGTCCGCGCGCGGACTTCGCCCTTTTCGTCGCCGCGGTACGCGTCCGCGGTCCNNTGAGC 60  
Db 63 CGTCCGCGCGCGGACGCGCGCTTTTCGTCGCCGCGGTACGCGTCCGCGGTCCACTGAGC 122  
Qy 61 GTGCGGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGGCGTGCCTGATGCG 120  
Db 123 GTGCGGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGGCGTCCGCTGATGCG 182  
Qy 121 CGCTTGGCGGNGATCGNCTCTTCATCCGCTNATCCCGACTTNCCTCAAGCCAGGATN 180  
Db 183 CGCTTGGCGGNGATCGCTCTCCATCCGCGTATCCCGACTTCCCAAGCCAGGATC 242  
Qy 181 ATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGNTCCGTGACACATATAC 240  
Db 243 ATGTTTCAGGACATCAGACGCTTGTCTCGATCCCAAGCGTCCGTGACACCATCGAC 302  
Qy 241 CATTTTGTCAAGCGGTACAGGACCAAGGNATCACCNWGGAAANTAGGATTAAGCTAG 300  
Db 303 CTCTTTGTCGAGCGGTACAAGGACCAAGGATCACCGTGTGCT--GGTGTGAAGCTAG 361  
Qy 301 AGGNTGTCATTTTCGGAACAACATNTCTTANAANNAATTTGGTCAAAAATGGTGCNATTT 360  
Db 362 AGGTTTCATTTTCGGTCTCTATCGCTT--TAGCCATCGCGCAAAAATTTGTGCCT-TT 418  
Qy 361 GAGGAAGCNAATNAGNTGCCANGCNAATAATGATTTTANGAATANGAATTTTNGGAATNN 420  
Db 419 GAGGAAGCGGAAGAAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTTGAATAT 476  
Qy 421 GGAATNTAGATAAAAAANT 440  
Db 477 GGAAGTGAAGAATAGATAAT 496  
RESULT 6  
US-09-865-419A-40126  
; Sequence 40126, Application US/09865419A  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Wu, Kunsheng

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51935)B  
; CURRENT APPLICATION NUMBER: US/09/865,419A  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/208,063  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 54020  
; SEQ ID NO 40126  
; LENGTH: 593  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3601-011-Pl-K6-A5  
US-09-865-419A-40126

Query Match 62.6%; Score 275.6; DB 33; Length 593;  
Best Local Similarity 79.1%; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGCGGACGCTTTCGCTTTCGCTCCCGCGGTGAGCGTCCGCGTCCNNTGAGC 60  
|||||  
Db 34 CGTCCGCGCGCGGACGCGCTTTCGCTCCCGCGGTGAGCGTCCGCGTCCACTGAGC 93  
|||||  
QY 61 GTCCGCGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGCGTNCGTGATGCG 120  
|||||  
Db 94 GTCCGCGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGCGTNCGTGATGCG 153  
|||||  
QY 121 CGCTTGGCGGNGATCGCTTCATCCNGGTNATNCCGACTTCCCAAGCCAGGGATN 180  
|||||  
Db 154 CGCTTGGCGGNGATCGCTTCATCCCGGTGATCCCGACTTCCCAAGCCAGGGATC 213  
|||||  
QY 181 ATGTTTCAGGACATCANGANGNTGNTTTCGATCCCAAGCGTCCGTGACACATATAC 240  
|||||  
Db 214 ATGTTTCAGGACATCAGGAGTTCGCTCGATCCCAAGCGTCCGTGACACATCGAC 273  
|||||  
QY 241 CATTTTGTCAAGCGGTACAGGACCAAGNATCACCTTGGAAATAGGAGTTAAAGCTAG 300  
|||||  
Db 274 CTCCTTGTGAGCGGTACAGGACCAAGGATCACCGGTGCT--GGTGTGAAGCTAG 332  
|||||  
QY 301 AGGNTCAATTTTCGGAACAACCTTANNTCTTANAANNAATTTGTCAAAATNGTGNCAAT 360  
|||||  
Db 333 AGGTTTCATTTTCGCTTCCTATCGCTT--TAGCCATCGCGGCAAAATTTGTCCT--TT 389  
|||||  
QY 361 GAGGAAGCNAATNAGTCCGANGCNAATGATTTTNGAATANGAATTTTNGGAATNN 420  
|||||  
Db 390 GAGGAAGCNAATNAGTCCGANGCNAATGATTTTNGAATANGAATTTTNGGAATAT 447  
|||||  
QY 421 GGAATNNTAGATAAAAAAT 440  
|||||  
Db 448 GGAACGTGACAGATAGAAAT 467

RESULT 7  
US-60-208-063-23182  
; Sequence 23182, Application US/60208063  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Lalquid, Raghunath V.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Shukla, Hridayabhiranjan  
; APPLICANT: Wu, Kunsheng  
; APPLICANT: Xu, Nanfei  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51935)A  
; CURRENT APPLICATION NUMBER: US/60/208,063  
; CURRENT FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 25021  
; SEQ ID NO 23182  
; LENGTH: 593

; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3601-011-Pl-K6-A5  
US-60-208-063-23182

Query Match 62.6%; Score 275.6; DB 64; Length 593;  
Best Local Similarity 79.1%; Pred. No. 5.2e-66;  
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGCGGACGCTTTCGCTTTCGCTCCCGCGGTGAGCGTCCGCGTCCNNTGAGC 60  
|||||  
Db 34 CGTCCGCGCGCGGACGCGCTTTCGCTCCCGCGGTGAGCGTCCGCGTCCACTGAGC 93  
|||||  
QY 61 GTCCGCGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGCGTNCGTGATGCG 120  
|||||  
Db 94 GTCCGCGTACCGCGCGGAGCGGAGCGGCGGTGGTGGCGATGCGTNCGTGATGCG 153  
|||||  
QY 121 CGCTTGGCGGNGATCGCTTCATCCNGGTNATNCCGACTTCCCAAGCCAGGGATN 180  
|||||  
Db 154 CGCTTGGCGGNGATCGCTTCATCCCGGTGATCCCGACTTCCCAAGCCAGGGATC 213  
|||||  
QY 181 ATGTTTCAGGACATCANGANGNTGNTTTCGATCCCAAGCGTCCGTGACACATATAC 240  
|||||  
Db 214 ATGTTTCAGGACATCAGGAGTTCGCTCGATCCCAAGCGTCCGTGACACATCGAC 273  
|||||  
QY 241 CATTTTGTCAAGCGGTACAGGACCAAGNATCACCTTGGAAATAGGAGTTAAAGCTAG 300  
|||||  
Db 274 CTCCTTGTGAGCGGTACAGGACCAAGGATCACCGGTGCT--GGTGTGAAGCTAG 332  
|||||  
QY 301 AGGNTCAATTTTCGGAACAACCTTANNTCTTANAANNAATTTGTCAAAATNGTGNCAAT 360  
|||||  
Db 333 AGGTTTCATTTTCGCTTCCTATCGCTT--TAGCCATCGCGGCAAAATTTGTCCT--TT 389  
|||||  
QY 361 GAGGAAGCNAATNAGTCCGANGCNAATGATTTTNGAATANGAATTTTNGGAATNN 420  
|||||  
Db 390 GAGGAAGCNAATNAGTCCGANGCNAATGATTTTNGAATANGAATTTTNGGAATAT 447  
|||||  
QY 421 GGAATNNTAGATAAAAAAT 440  
|||||  
Db 448 GGAACGTGACAGATAGAAAT 467

RESULT 8  
US-10-219-999-25058  
; Sequence 25058, Application US/10219999  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Stein, Joshua  
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-10(52726)C  
; CURRENT APPLICATION NUMBER: US/10/219,999  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 60/324,109  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: US 60/312,544  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 63520  
; SEQ ID NO 25058  
; LENGTH: 892  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(697)  
; OTHER INFORMATION:  
US-10-219-999-25058

Query Match 62.6%; Score 275.6; DB 42; Length 892;  
Best Local Similarity 79.1%; Pred. No. 6.1e-66;

Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGGACATTCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 60  
DB 53 CGTCCGCGCGGACGACGCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCACTGAGC 112  
QY 61 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 113 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 172  
QY 121 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 180  
DB 173 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 232  
QY 181 ATGTTTCAGGACATCANGANGTGTGCTTCGATCCCAAGCGGTCGCTGACACATATAC 240  
DB 233 ATGTTTCAGGACATCAGACGCTTCTCTCTATCGCTT--TAGCCATCGCGCAAAATTTGTGCCT-TT 292  
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 300  
DB 293 CTCCTTGTTCGAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 351  
QY 301 AGGNTCANTTTCCGACCAACTANNTCTTANAANNAATTTGTCACAAATNGGTGNCNATT 360  
DB 352 AGGNTCANTTTCCGACCAACTANNTCTTANAANNAATTTGTCACAAATNGGTGNCNATT 408  
QY 361 GAGGAAGCNAATNAGTGGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
DB 409 GAGGAAGCNAATNAGTGGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 466  
QY 421 GGAATNTAGATAAAAAAT 440  
DB 467 GGAATNTAGATAAAAAAT 486

RESULT 9  
US-09-865-439A-27582  
; Sequence 27582, Application US/09865439A  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hardeman, Kristine J.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(51936)B  
; CURRENT APPLICATION NUMBER: US/09/865,439A  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 119126  
; SEQ ID NO 27582  
; LENGTH: 626  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3354-015-P1-K1-A8  
US-09-865-439A-27582

Query Match 60.8%; Score 267.6; DB 33; Length 626;  
Best Local Similarity 78.0%; Pred. No. 9.1e-64;  
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGGACATTCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 60  
DB 6 CGTCCGCGCGGACGACGCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCACTGAGC 65  
QY 61 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 66 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 125  
QY 121 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 180  
DB 126 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCACTGAGC 185  
QY 181 ATGTTTCAGGACATCANGANGTGTGCTTCGATCCCAAGCGGTCGCTGACACATATAC 240  
DB 186 ATGTTTCAGGACATCAGACGCTTCTCTCTATCGCTT--TAGCCATCGCGCAAAATTTGTGCCT-TT 292  
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 300  
DB 293 CTCCTTGTTCGAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 351

QY 181 ATGTTTTCAGGACATCANGANGTGTGCTTCGATCCCAAGCGGTCGCTGACACATATAC 240  
DB 186 ATGTTTTCAGGACATCAGACGCTTCTCTCTATCGCTT--TAGCCATCGCGCAAAATTTGTGCCT-TT 361  
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 300  
DB 246 CTCCTTGTTCGAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 304  
QY 301 AGGNTCANTTTCCGACCAACTANNTCTTANAANNAATTTGTCACAAATNGGTGNCNATT 360  
DB 305 AGGNTCANTTTCCGACCAACTANNTCTTANAANNAATTTGTCACAAATNGGTGNCNATT 361  
QY 361 GAGGAAGCNAATNAGTGGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
DB 362 GAGGAAGCNAATNAGTGGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 419  
QY 421 GGAATNTAGATAAAAAAT 440  
DB 420 GGAATNTAGATAAAAAAT 439

RESULT 10  
US-60-207-458-71879  
; Sequence 71879, Application US/60207458  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Deikman, Jill  
; APPLICANT: Hardeman, Kristine J.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Lalquid, Raghunath V.  
; APPLICANT: Ruan, Yijun G.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Sammons, R. Douglas  
; APPLICANT: Shukla, Hridayabhiranjan  
; APPLICANT: Xu, Nanfei  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI  
; FILE REFERENCE: 38-21(51936)A  
; CURRENT APPLICATION NUMBER: US/60/207,458  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 152403  
; SEQ ID NO 71879  
; LENGTH: 626  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3354-015-P1-K1-A8  
US-60-207-458-71879

Query Match 60.8%; Score 267.6; DB 64; Length 626;  
Best Local Similarity 78.0%; Pred. No. 9.1e-64;  
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGGACATTCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 60  
DB 6 CGTCCGCGCGGACGACGCGCTTTTCGTCCTCCCGCGTCAGCGTCGGGCTCCACTGAGC 65  
QY 61 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 66 GTGCGCGTCACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 125  
QY 121 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCNNTGAGC 180  
DB 126 CGCTTGGCGGAGTCGCTTCCTTCGTCCTCCCGCGTCAGCGTCGGGCTCCACTGAGC 185  
QY 181 ATGTTTTCAGGACATCANGANGTGTGCTTCGATCCCAAGCGGTCGCTGACACATATAC 240  
DB 186 ATGTTTTCAGGACATCAGACGCTTCTCTCTATCGCTT--TAGCCATCGCGCAAAATTTGTGCCT-TT 361  
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 300  
DB 293 CTCCTTGTTCGAGCGGTACAAGGACCAAGGATACACCTTTCGATCCCAAGCGGTCGCTGACACATATAC 351



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Db 246 CTCCTTGTGAGCGGTCACAGGACCAAGGATCACCGTGGTGGCT-GGTGTTGAAGCTAG 304
QY 301 AGGNTCANTTTCCGAACAACCTANNCTTTANANNAATTTGGTCAAAAATNGGTGNCNATT 360
Db 305 AGGTTTCATTTTGGTCCCTCCATCCGCTT--TAGCCATTGGCGCAAAATTTGTGCT--TT 361
QY 361 GAGGAACNNAATNAGTCCGAGCAATAGATTTTANAGATATANGAATTTTNGGAATNN 420
Db 362 GAGGAAGCGGAAGAGTTGCCAGCGAGGTGATCT--CCGAAGATATTCTTTTGGAAATAT 419
QY 421 GGAATNTAGATAAAAAAT 440
Db 420 GGAATNTAGATAAAAAAT 439

RESULT 11
US-09-696-664A-10668
; Sequence 10668, Application US/09696664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 10668
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(640)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: L1B3279-182-Q1-K6-A2
US-09-696-664A-10668

Query Match 60.8%; Score 267.6; DB 27; Length 640;
Best Local Similarity 78.0%; Pred. No. 9,1e-64;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;
QY 1 CGTCCGCGCGCGGACTTCGCTTTTGTCCCGGCTCAGCGTCGCGGCTCCNNTGAGC 60
Db 6 CGTCCGCGCGCGCGGACTTCGCTTTTGTCCCGGCTCAGCGTCGCGGCTCCACTGAGC 65
QY 61 GTGCGCGTCACCGCGGAGGAGGAGGCGGTGGTGGCGATGCGCTGATGCG 120
Db 66 GTGCGGTGTACCGCGGAGGAGGAGGAGGCGGTGGTGGCGATGCGCTGAGCGG 125
QY 121 CGCTTGGCGGAGATCGCTTCCTTCATCCNGGTATNCCGACTTCCCAAGCCAGGGATN 180
Db 126 CGCTTGGCGGAGATCGCTTCCTTCATCCCGCTCCCGGACTTCCCAAGCCAGGGATC 185
QY 181 ATGTTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGGCTCCGTGACAAATATAC 240
Db 186 ATGTTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGGCTCCGTGACAAATATAC 245
QY 241 CATTTTGTCAAGCGGTACAAAGCAACAGGATCAACNNTAGGAATAGGAGTTAAAGCTAG 300
Db 246 CTCCTTGTGACGCGGTACAAAGCAACAGGATCAACNNTAGGAGTTAAAGCTAG 304
QY 301 AGGNTCANTTTCCGAACAACCTANNCTTTANANNAATTTGGTCAAAAATNGGTGNCNATT 360
Db 305 AGGTTTCATTTTGGTCCCTCCATCCGCTT--TAGCCATTGGCGCAAAATTTGTGCT--TT 361
QY 361 GAGGAACNNAATNAGTCCGAGCAATAGATTTTANAGATATANGAATTTTNGGAATNN 420
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Db 362 GAGGAAGCGCAAGAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTGGAATAT 419
QY 421 GGAATNTAGATAAAAAAT 440
Db 420 GGAATNTAGATAAAAAAT 439

RESULT 12
US-10-219-999-7177
; Sequence 7177, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 7177
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(656)
; OTHER INFORMATION:
US-10-219-999-7177

Query Match 60.8%; Score 267.6; DB 42; Length 961;
Best Local Similarity 78.0%; Pred. No. 1,1e-63;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;
QY 1 CGTCCGCGCGCGGACTTCGCTTTTGTCCCGGCTCAGCGTCGCGGCTCCNNTGAGC 60
Db 12 CGTCCGCGCGCGGACTTCGCTTTTGTCCCGGCTCAGCGTCGCGGCTCCACTGAGC 71
QY 61 GTGCGCGTCACCGCGGAGGAGGAGGCGGTGGTGGCGATGCGCTGATGCG 120
Db 72 GTGCGGTGTACCGCGGAGGAGGAGGCGGTGGTGGCGATGCGCTGAGCG 131
QY 121 CGCTTGGCGGAGATCGNCTCCCTNCATCCNGGTATNCCGACTTCCAAAGCCAGGGATN 180
Db 132 CGCTTGGCGGAGATCGNCTCCCTNCATCCNGGTATNCCGACTTCCAAAGCCAGGGATC 191
QY 181 ATGTTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGGCTCCGTGACAAATATAC 240
Db 192 ATGTTTTCAGGACATCANGANGNTGTTTCGATCCCAAGCGGCTCCGTGACAAATATAC 251
QY 241 CATTTTGTCAAGCGGTACAAAGCAACAGGATCAACNNTAGGAATAGGAGTTAAAGCTAG 300
Db 252 CTCCTTGTGAGCGGTACAAAGCAACAGGATCAACNNTAGGAATAGGAGTTAAAGCTAG 310
QY 301 AGGNTCANTTTCCGAACAACCTANNCTTTANANNAATTTGGTCAAAAATNGGTGNCNATT 360
Db 311 AGGTTTCATTTTGGTCCCTCCATCCGCTT--TAGCCATTGGCGCAAAATTTGTGCT--TT 367
QY 361 GAGGAACNNAATNAGTCCGAGCAATAGATTTTANAGATATANGAATTTTNGGAATNN 420
Db 368 GAGGAAGCGGAAGAGTTGCCAGCGAGGTGATCT--CCGAAGAGTATTCTTTGGAATAT 425
QY 421 GGAATNTAGATAAAAAAT 440
Db 426 GGAATNTAGATAAAAAAT 445
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RESULT 13
US-60-312-544-3121
; Sequence 3121, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 3121
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(656)
; OTHER INFORMATION: Clone ID: LIB3068-059-H7_FLI
US-60-312-544-3121

Query Match          60.8%; Score 267.6; DB 75; Length 961;
Best Local Similarity 78.0%; Pred. No. 1.1e-63;
Matches 343; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

QY 1 CGTCCGCGCGCGCGACTTCGCTTTTCGTCGCCGCGTCAGCGTCCGCGGTCCTCCTGAGC 60
DB 12 CGTCCGCGCGCGCGCGCGCTTTTCGTCGCCGCGTCAGCGTCCGCGGTCCTCCTGAGC 71
QY 61 GTGCGCGTCACCGCGCGCGAGGCGAGCGGTGTGCGGTCGATGGGTGCGTGTGATGCG 120
DB 72 GTGCGGTGTACCGCGCGCGGAGGCGAGGCGGTGTGCGGTCGATGGGTGCGTGTGATGCG 131
QY 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCACAAAGCCAGGATN 180
DB 132 CGCTTGGCGGNGATCGCTCCTCCATCCGCGTCATCCCGGACTTCCCAAGCCAGGATC 191
QY 181 ATGTTTCAGGACATCANGANGTGTGTCATCCGAGCGGTCGATCCGTCGACACATATAC 240
DB 192 ATGTTTCAGGACATCAGGAGTGTGCTGTCATCCCAAGCGGTCGTCGTCACCATCGAC 251
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTGGAATAGGATTAAGCTAG 300
DB 252 CTCTTTGTGAGCGGTACAAGGACCAAGGATACACCTGTCGT-TTGGCT-TTGGCT-TT 310
QY 301 AGGNTCANTTTTGGTCTCTATCGCTT--TAGCCATTTGGCGCAAAATTTTGGCT-TT 360
DB 311 AGGNTCANTTTTGGTCTCTATCGCTT--TAGCCATTTGGCGCAAAATTTTGGCT-TT 367
QY 361 GAGGAAGCNAATNAGTCCGAGCNAATATTTTANAAATTTGTCATAAATNGGTGCTGCT 420
DB 368 GAGGAAGCNAATNAGTCCGAGCNAATATTTTANAAATTTGTCATAAATNGGTGCTGCT 425
QY 421 GGAATNTAGATAAATAAANT 440
DB 426 GGAAGTGAAGATAGAAAT 445

RESULT 14
US-09-513-996A-69703
; Sequence 69703, Application US/09513996A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-709P
; CURRENT APPLICATION NUMBER: US/09/513,996A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 81028

; SEQ ID NO 69703
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 1..462
; OTHER INFORMATION: any n or Xaa = unknown
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US-09-513-996A-69703

Query Match          60.4%; Score 265.8; DB 19; Length 462;
Best Local Similarity 79.5%; Pred. No. 2.5e-63;
Matches 337; Conservative 0; Mismatches 81; Indels 6; Gaps 4;

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DB 42 CGTCCGCGCGCGCGCGCGCTTTTCGTCGCCGCGTCAGCGTCCGCGGTCCTCCTGAGC 101
QY 61 GTGCGCGTCACCGCGCGCGAGGCGAGGCGGTGTGCGGTCGATGGGTGCGTGTGATGCG 120
DB 102 GTGCGGTGTACCGCGCGCGAGGCGAGGCGGTGTGCGGTCGATGGGTGCGTGTGATGCG 161
QY 121 CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCACAAAGCCAGGATN 180
DB 162 CGCTTGGCGGNGATCGCTCCTCCATCCGCGTCATCCCGGACTTCCCAAGCCAGGATC 221
QY 181 ATGTTTCAGGACATCANGANGTGTGTCATCCCAAGCGGTCGATCCGTCGACACATATAC 240
DB 222 ATGTTTCAGGACATCAGGAGTGTGTCGTCGATCCCAAGCGGTCGTCGTCGACACATCAG 281
QY 241 CATTTTGTCAAGCGGTACAAGGACCAAGGATACACCTGGAATAGGATTAAGCTAG 300
DB 282 CTCTTTGTGAGCGGTACAAGGACCAAGGATACACCTGTCGT-TTGGCT-TTGGCT-TT 340
QY 301 AGGNTCANTTTTGGTCTCTATCGCTT--TAGCCATTTGGCGCAAAATTTTGGCT-TT 360
DB 341 AGGNTCANTTTTGGTCTCTATCGCTT--TAGCCATTTGGCGCAAAATTTTGGCT-TT 397
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DB 456 GGAA 459

RESULT 15
US-09-865-439A-82458
; Sequence 82458, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
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; TYPE: DNA
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Query Match          60.1%; Score 264.4; DB 33; Length 572;
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| Db   | 29  | CGTCGGCGCGCGCGCGCGCGCTTCCTTCCTCCCGCGCTCAGCGTCGCGGCTCCACTGAGC          | 88  |
| Qy   | 61  | GTGCGCGTCACCGCGCGCGCGCGCGCGCGCTTCCTTCCTCCCGCGCTCAGCGTCGCGGCTCCACTGAGC | 120 |
| Db   | 89  | GTGCGCGTCACCGCGCGCGCGCGCGCGCGCTTCCTTCCTCCCGCGCTCAGCGTCGCGGCTCCACTGAGC | 148 |
| Qy   | 121 | CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATCCCGACTTCCAAAGCCAGGATN             | 180 |
| Db   | 149 | CGCTTGGCGGNGATCGNCTCCTNCATCCCGACTTCCAAAGCCAGGATN                      | 208 |
| Qy   | 181 | ATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGNTCCGTGACAAATATAC              | 240 |
| Db   | 209 | ATGTTTCAGGACATCANGANGNTGNTGTCATCCCAAGCGNTCCGTGACAAATATAC              | 268 |
| Qy   | 241 | CATTTCGTCAGCGGTACAGGACCAAGGATCACCNTGGAAANTAGGAGTTAAAGCTAG             | 300 |
| Db   | 269 | CTCTTTGTCAGCGGTACAGGACCAAGGATCACCNTGGAGTTAAAGCTAG                     | 327 |
| Qy   | 301 | AGGGNTCANTTTCGGAACAACATNTCTTANAANNAATGGTCAAAATNGTGNCNATT              | 360 |
| Db   | 328 | AGGGTTCATTTTGGTCTCTCTATCGCT--TAGCCATTGGCGCAAAATTTGTGCT--TT            | 384 |
| Qy   | 361 | GAGGAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATTTNGGAATNN                | 420 |
| Db   | 385 | GAGGAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATTTNGGAATNN                | 442 |
| Qy   | 421 | GGAATNTAGATAAAAAANT   | 440 |
| Db   | 443 | GGAATNTAGATAAAAAANT   | 462 |

Search completed: November 30, 2002, 05:07:19  
Job time : 3372 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 02:40:12 ; Search time 267 Seconds  
(without alignments)  
3711.158 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtcgcgcgcgcgcgcgcctc.....ggaaatntagataaaaaant 440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
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| 1          | 265.8 | 60.4        | 462    | 21 AAC51765 | Zea mays DNA fragm |
| 2          | 225   | 51.1        | 455    | 21 AAC51740 | Zea mays DNA fragm |
| 3          | 93.6  | 22.6        | 405    | 21 AAC43563 | Zea mays DNA fragm |
| 4          | 90.4  | 20.5        | 380    | 21 AAA31767 | Plant Microsatelli |
| 5          | 88.4  | 20.1        | 1034   | 21 AAC49172 | Arabidopsis thalia |
| 6          | 88.4  | 20.1        | 1036   | 21 AAC35980 | Arabidopsis thalia |
| 7          | 88.2  | 20.0        | 729    | 14 AAQ35208 | Sequence encoding  |
| 8          | 86.8  | 19.7        | 1036   | 21 AAC40946 | Arabidopsis thalia |
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| 10   | 85   | 19.3 | 780     | 21 AAC40942 | Arabidopsis thalia |
| 11   | 85   | 19.3 | 821     | 21 AAC40945 | Arabidopsis thalia |
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| 16   | 69   | 15.7 | 579     | 21 AAC44711 | Arabidopsis thalia |
| 17   | 67.8 | 15.4 | 372     | 21 AAC46302 | Arabidopsis thalia |
| 18   | 67.8 | 15.4 | 1337    | 21 AAC45318 | Arabidopsis thalia |
| 19   | 67.8 | 15.4 | 1348    | 21 AAC34911 | Arabidopsis thalia |
| 20   | 63.8 | 14.5 | 945     | 24 ABN98579 | Arabidopsis thalia |
| 21   | 43.6 | 9.9  | 376     | 22 AA559140 | Human immune/hema  |
| 22   | 40.2 | 9.1  | 18477   | 23 AA559634 | Propionibacterium  |
| c 23 | 39   | 8.9  | 109519  | 22 AA508693 | Micromonospora DNA |
| c 24 | 38.2 | 8.7  | 390     | 24 ABN21436 | Human ORFX polynuc |
| 25   | 38.2 | 8.7  | 2803    | 22 AAH54984 | S. epidermidis gen |
| c 26 | 38.2 | 8.7  | 3002    | 22 AAH54052 | S. epidermidis gen |
| 27   | 38   | 8.6  | 7178    | 21 AAH59145 | Actinoplanes sp. a |
| 28   | 37.4 | 8.5  | 17955   | 19 AAV56642 | Human immune syste |
| 29   | 37.2 | 8.5  | 6072    | 24 AB132030 | DNA encoding novel |
| c 30 | 36.8 | 8.4  | 423     | 23 AAS72516 | DNA encoding novel |
| c 31 | 36.8 | 8.4  | 423     | 23 AAS91898 | DNA encoding novel |
| c 32 | 36.8 | 8.4  | 4403765 | 22 AAI99683 | Mycobacterium tube |
| c 33 | 36   | 8.2  | 469     | 21 AAC38332 | Zea mays DNA fragm |
| c 34 | 36   | 8.2  | 2464    | 23 AAS86119 | DNA encoding novel |
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| 36   | 35   | 8.0  | 888     | 22 AAH51974 | Mycobacterium tube |
| 37   | 35   | 8.0  | 888     | 24 ABK14303 | DNA encoding proli |
| 38   | 35   | 8.0  | 2209    | 24 ABK14301 | DNA encoding proli |
| 39   | 35   | 8.0  | 5181    | 24 ABL68935 | Kidney cancer rela |
| 40   | 35   | 8.0  | 4403765 | 22 AAI99683 | Mycobacterium tube |
| 41   | 35   | 8.0  | 4411529 | 22 AAI99682 | Mycobacterium tube |
| c 42 | 34.8 | 7.9  | 3076    | 19 AAVA3674 | Receptor type tyro |
| c 43 | 34.8 | 7.9  | 3441    | 18 AAT87922 | Rat cerebellum der |
| c 44 | 34.8 | 7.9  | 65140   | 22 AAD17184 | Streptomyces nous  |
| c 45 | 34.8 | 7.9  | 125401  | 22 AAD17186 | Streptomyces nous  |

#### ALIGNMENTS

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AC AAC51765;  
XX  
AC AAC51765;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Zea mays DNA fragment SEQ ID NO: 69703.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EPI033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
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PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
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Query Match 60.4%; Score 265.8; DB 21; Length 462;  
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| PR | 08-JUL-1999; | 99US-0142920.  | PR  | 24-SEP-1999; | 99US-0155659. |
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| PR | 30-AUG-1999; | 99US-0151303.  |   |              |               |
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|    |              |  | Query Match 51.1%; Score 225; DB 21; Length 455;              |              |               |
|    |              |  | Best Local Similarity 75.0%; Pred. No. 4.8e-55;               |              |               |
|    |              |  | Matches 282; Conservative 0; Mismatches 90; Indels 4; Gaps 2; |              |               |
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| Db | 84           | CGCCTTTTCGTCCCGCGTCGCGGCTCGCGGCTCGCGGCTACGCGTACCGGGGAA 143       |   |              |               |
| QY | 80           | GCGGAGGCGCGGTGGTGGCGATGCGGTCGATGCGGCTGGCGGATCGNCT 139            |   |              |               |
| Db | 144          | GCGGAGGCGCGGTGGTGGCGATGCGGTCGCGGACGCGGCTGGCGGGGATTCCT 203        |   |              |               |
| QY | 140          | CTTCATCCNGGTNATCCCGACTTCCAAAGCAGGAGATNATGTTTCAGGACATCANGA 199    |   |              |               |
| Db | 204          | CTTCATCCCGGTATCCCGACTTCCCAAGCAGGAGATCATGTTCCAGGACATCAGCA 263     |   |              |               |
| QY | 200          | NGNTGNTTTCGATCCCAAGCGNTCCGTGACACATATACCATTTTGTCAACGGTACA 259     |   |              |               |
| Db | 264          | CACCTGCTCTGACCCCAAGCGTTCGGTGACACCATCGAGCTCTTCGTTGAGCGGTACA 323   |   |              |               |
| QY | 260          | AGGACCAAGGNATCACCNNTGGAANTAGGATTAAGCTAGAGGNTCANTTTCGGAACA 319    |   |              |               |
| Db | 324          | AGGACCAAGGATCACCGTAGTTGCT-GGTGTGGAAGCTAGAGGTTTCATTTTGTCT 382     |   |              |               |
| QY | 320          | ACTANNTCTTANAANNAATTTGTCAAAAATNGGTGNCNATTTGAGAGAGCNNAATNAGTG 379 |   |              |               |
| Db | 383          | CCATCGCTCTAGCCATCAGTGCAGAAATTTG---TACCTTTGAGGAAGCCTAAGAGTTG 439  |   |              |               |



QY 380 CCANGCNAATGATTT 395  
    | | | | | | | | | |  
Db 440 CCAGCGAGGTGATCT 455

RESULT 3  
ID AAC43563 standard; DNA; 405 BP.  
XX  
AC AAC43563;  
XX  
DT 17-OCT-2000 (first entry)  
DE  
ZE Zea mays DNA fragment SEQ ID NO: 39686.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 22.6%; Score 99.6; DB 21; Length 405;
Best Local Similarity 83.8; Pred. No. 7.5e-19;
Matches 114; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 1 CGTCCGCGCGCGGACTTCGCCCTTTTCGTCCCGCGCTCAGCGTCGGGCTCCNNTGAGC 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 CGTCCGCGCGCGGACGCCGCTTTTCGTCCCGCGCTCASS--YCGCGCTCCACTGAGC 82
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GTGCGCGTCAACCGCGGCGGAGCGCGTGTGGCGGATGGCGTNCGCTGATGCG 120
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Db 83 GTCCGTGTCAACCGCGGCGGAGGCAAGGCGGCGGTGGTGGCGATGGCTCCGCTGACSSG 142
QY 121 CGCTTGGCGGNGATCG 136
      |||||:|||||:|||||
Db 143 CGCTTGGCGGCGGATG 158
      |||||:|||||:|||||

RESULT 4
AAA31767
ID AAA31767 standard; DNA; 380 BP.
XX
AC AAA31767;
XX
DT 05-JUL-2000 (first entry)
XX
DE Plant microsatellite marker #728.
XX
KW Plant microsatellite sequence; core repeat sequence; detection; probe;
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
PN WO9967421-A1.
XX
PD 29-DEC-1999.
XX
PF 25-JUN-1999; 99WO-NZ00092.
XX
PR 25-JUN-1998; 98US-0105307.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Havukkala IJ, Bloksberg LN, Glenn M;
XX
DR WPI; 2000-116958/10.
XX
PT New plant microsatellite markers and associated flanking species for
PT the detection of polymorphic genetic markers -
XX
PS Claim 1; Page 291; 392pp; English.
XX
CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC and associated flanking species. The sequences comprise a central core
CC repeat sequence, especially selected from the sequences AAA32094-A32096
CC with left and right flanking sequences. The polynucleotide sequences
CC can be used in the detection of DNA polymorphisms, in genome mapping,
CC in physical mapping, in positional cloning of genes, in variety
CC identification and in evaluation of genetic variability within and
CC between plant tissues, populations, cultivars, species and species
CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are
CC useful to locate specific economically useful genes in plant genomes.
XX
SQ Sequence 380 BP; 76 A; 103 C; 88 G; 113 T; 0 other;

Query Match 20.5%; Score 90.4; DB 21; Length 380;
Best Local Similarity 57.0%; Pred. No. 3.3e-16;
Matches 142; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 81 GCGAGGCGAGCGGTGGTGGCGATGGCTNCGGTGATGCGCGTTCGGCGNGATCNCNCTC 140
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 GCGAGATCAACATCGCGTCCCAAGGCGGTGAGGACCTCGTCTCGCCAAGATCGCCTC 169
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 141 CTNATCCNGGTATNCCCGACTTNCARAGCCAGGATNATGTTTCAGACATCANGAN 200
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 170 TTCGATCCGGTCAATCCAGATTTCGCCAAGCCAGGATATGTTTCAGGATATAACGAC 229
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 201 GNTGNTCTTCGATCCCAAGCGGNTCCGTGACAAACATATACCATTTTGTCAAGCGGTACAA 260
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 230 GTTGTCTTCTTAATCCTGAGGCGTTTAAAGTACTATTGATCTCTTTGTCAGAGGTACAG 289
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
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PR 26-OCT-1999; 99US-0161359.  
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PR 26-OCT-1999; 99US-0161361.  
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| DB                        | 103  | GATCCAGAAATCGCTAAAGATTGCTTCCCATTAGAGTCATCCCGGACTTCCCTAAACCA 162   |
| QY                        | 175  | GGGATNATGTTTCAGGACATCANGANGTGNMTGTTCGATCCCAAGGCCNTCCGTGACAAAC 234 |
| DB                        | 163  | GGAATCATGTTTCAGGACATCAACGACGCTTCTTCGACATGAGGCCCTTAAAGGATACT 222   |
| QY                        | 235  | ATATACCATTTTGTCAAGCGGTACAAGCAAGCAACGATACACNTGGAAANTFAGGAGTTAA 294 |
| DB                        | 223  | ATTGCTTTGTTGTGTAGATACAAAGATAAAGGCATATCTGTG-TTGCAGGTGTTGA 281      |
| QY                        | 295  | AGCTAGAGGNTCNTTTTCGGAACAACATNNTCTTANANNAATTTGGTCAAAATNGGTG 354    |
| DB                        | 282  | AGCTAGAGGTTTCATTTTGGCCCTCCTATTGCGTGTG--GCTATTGGTGCCAAATTTGTT 339  |
| QY                        | 355  | NCNATTGAGGAGCNAATNAGNTGCCANGCNAATGATTTTNANGAATANGAATTTTNG 414     |
| DB                        | 340  | CCCA-TGAGGAGCGCCCAAGAGTACCTGGGAGGTTATTTCGGAGGAGTATTCGTTGGA 398    |
| QY                        | 415  | GAATNNGAANTNAGATAAAA 437  |
| DB                        | 399  | GTATGGACCAGATACGATTGAGA 421                                       |
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| AAC43276                  |  |   |
| ID                        | AAC43276 standard; DNA; 552 BP.                                |   |
| XX                        | AC   | AAC43276;   |
| XX                        | XX   |   |
| DT                        | 17-OCT-2000 (first entry)                                      |   |
| XX                        | XX   |   |
| DE                        | Arabidopsis thaliana DNA fragment SEQ ID NO: 38674.            |   |
| XX                        | XX   |   |
| KW                        | Hybridisation assay; genetic mapping; gene expression control; |   |
| KW                        | protein identification; signal transduction pathway;           |   |
| XX                        | metabolic pathway; promoter; termination sequence; ss.         |   |
| XX                        | OS   | Arabidopsis thaliana.   |
| XX                        | XX   |   |
| PN                        | EP1033405-A2.  |   |
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| PD                        | 06-SEP-2000.   |   |
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| PR        | 28-OCT-1999;   | 99US-0161992.   |                       |              |                    |                 |             | PR | 11-MAY-1999; |
| PR        | 29-OCT-1999;   | 99US-0162142.   |                       |              |                    |                 |             | PR | 14-MAY-1999; |
| Qy        | 115  | GATGCGCCCTTGGCGNGGATGNCCTCTNCATCCNGGTNATNCCGGACTTNCCAAAGCCA     | 174                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Db        | 178  | GATCCTCTCGTATCCATGGAAATCAAACTAAGATCCGTGCTTCCAGATTTTCCCAAGAAA    | 237                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Qy        | 175  | GGGATNATGTTTTCAGGACATCANGANGTNGTGTTCGATCCCAAGCGGTCGGTGACAAC     | 234                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Db        | 238  | GGAAATAGTTTCAAGACATACACACAGTGTGTGGATCCGAAAGCCTTCAAAACACACA      | 297                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Qy        | 235  | ATATACCAATTTGTCAAGGGGTACAGGACCAAGNATCACCTTGAANTAGGAGTTAA        | 294                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Db        | 298  | ATTGATCTGTTTGTGGAGAGGTACAGACAAAGAAACATCTCAGTGG-TTGCAGGAATAGA    | 356                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Qy        | 295  | ACCTAGAGGGTTCANTTTCGGAACAACACTANNTCTTANAANNAATTTGGTCAAAAATNGGTG | 354                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Db        | 357  | GGCTCGTGGTTTCCATTTCGGTGCACCGA--TCGGGCTAGCCATTGGAGCAAAATTTGTT    | 414                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Qy        | 355  | NCNATTGAGGAACGNNAAATNAGTNGCCANGCNAATGATTTTNNANGAATANGAATTT      | 410                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| Db        | 415  | CCTCTCGCCAAACCCAGAAACTACCTGGTGAACAATATTTTGAGGAATACGAGTT         | 470                   | (((((        | (((((              | (((((           | (((((       | PR | 14-MAY-1999; |
| RESULT 14 |  |   |                       |              |                    |                 |             |    |              |
| AAC46344  |  |   |                       |              |                    |                 |             |    |              |
| ID        | AAC46344 standard; DNA; 459 BP.                                |   |                       |              |                    |                 |             |    |              |
| XX        | AAC46344;  |   |                       |              |                    |                 |             |    |              |
| AC        |  |   |                       |              |                    |                 |             |    |              |
| XX        | 18-OCT-2000 (first entry)                                      |   |                       |              |                    |                 |             |    |              |
| DE        | Arabidopsis thaliana DNA fragment SEQ ID NO: 49794.            |   |                       |              |                    |                 |             |    |              |
| XX        |  |   |                       |              |                    |                 |             |    |              |
| KW        | Hybridisation assay; genetic mapping; gene expression control; |   |                       |              |                    |                 |             |    |              |
| KW        | protein identification; signal transduction pathway;           |   |                       |              |                    |                 |             |    |              |
| KW        | metabolic pathway; promoter; termination sequence; ss.         |   |                       |              |                    |                 |             |    |              |
| XX        | Arabidopsis thaliana.  |   |                       |              |                    |                 |             |    |              |
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## TITLE

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## COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

----- Project Information

Center project name: KBZR

Center clone name: CH230-430L22

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 95541 bases at least Q40  
Consensus quality: 98821 bases at least Q30  
Consensus quality: 100748 bases at least Q20

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\* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 43 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 1025: contig of 1025 bp in length

\* 1026 1125: gap of unknown length

\* 1126 2386: contig of 1261 bp in length

\* 2387 2486: gap of unknown length

\* 2487 3784: contig of 1298 bp in length

\* 3785 3884: gap of unknown length

\* 3885 5017: contig of 1133 bp in length

\* 5017 5117: gap of unknown length

\* 5118 6832: contig of 1715 bp in length

\* 6833 8425: gap of unknown length

\* 8426 8525: gap of unknown length

\* 8526 9891: contig of 1366 bp in length

\* 9892 9991: gap of unknown length

\* 9992 11179: contig of 1188 bp in length

\* 11180 13126: contig of 1847 bp in length

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\* 13227 14729: contig of 1503 bp in length

\* 14730 14829: gap of unknown length

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\* 17351 19668: gap of unknown length

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\* 21277 21376: gap of unknown length

\* 21377 22520: contig of 1144 bp in length

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\* 24871 26573: contig of 1703 bp in length

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Query Match 4.5%; Score 20; DB 2; Length 128875;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CGGAGCGGAGGCGGCGG 94  
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 Db 5568 CGGAGCGGAGGCGGCGG 5549

# RESULT 2

AE012058 Xanthomonas axonopodis pv. citri str. 306, linear BCT 29-MAY-2002  
 the complete genome.  
 AE012058 AE008923  
 AE012058.1 GI:211110507  
 Xanthomonas axonopodis pv. citri str. 306.  
 Xanthomonas axonopodis pv. citri str. 306  
 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 Xanthomonas.

1 (bases 1 to 10525)  
 da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,  
 Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida  
 Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,  
 Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,  
 Chabergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,  
 Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,  
 Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C.,  
 Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite  
 Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,  
 Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,  
 Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,  
 Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A.,  
 Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,  
 Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos  
 Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and  
 Kitajima,J.P.

Comparison of the genomes of two Xanthomonas pathogens with

# TITLE

# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

differing host specificities  
 Nature 417 (6887), 459-463 (2002)  
 22022145  
 12024217  
 2 (bases 1 to 10525)  
 da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,  
 Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida  
 Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,  
 Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,  
 Chabergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,  
 Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,  
 Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C.,  
 Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite  
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 Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,  
 Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,  
 Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.,H.A.,  
 Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,  
 Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos  
 Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and  
 Kitajima,J.P.

# TITLE JOURNAL

Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de  
 Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,  
 Brazil

# FEATURES

source

Location/Qualifiers  
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 /db\_xref="taxon:190486"  
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CDS

gene

CDS

gene

CDS

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DPTMELHLADTLQAAAMPRTNDFDRAGTSALLIVQTRAGDPDPTGOOLAYDAVQ
AAFAVSKGTATRLTLTPGCAFAVEITARTQGEAQWIGTLDVGLVLLLVAYRSWKI
PVLGVLPASAGLAGLGAVALFLFDGVHGITVAFGFTLIGVVODYPIHLFSHORPGLDP
RENARHMLTLAGVYSTCIAYVTFELFSGVDGLRQLAVFTTAGLATAVTTTRMLPAL
IDPAPRDYADSVLAVLMRGIAARLPRIISLAAMAVIGTAVTFAPGQFWONDLSKLT
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APLLPKOLSGPLATSVGLLGRGDRSTALVSLGLRDPVAVLAAYVGSQNLIDLK
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GTGVENLPHLIALALAGLQDLYALFFDHAGDDHADQDLTHALIVCSLMTLLVFAL
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NPQLAANIIDAGMDATSIYMAIKATDAGALVALIDPRREGDPALPAMFTGRNMFPP
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/note="identified by sequence similarity; putative; ORF
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Query Match

Best Local Similarity 4.3%; Score 19; DB 1; Length 10525;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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IIIIIIIIIIIIIIIIIIIIII

Db 10245 GCAGCGCGTGTGGCGGATG 10263

RESULT 3

AC078977

LOCUS

DEFINITION

Oryza sativa chromosome 5 clone P0496H07, linear HTG 23-JUN-2001

PROGRESS \*\*\*, 8 unordered pieces.

AC078977

AC078977.2 GI:14530829

HTG: HTGS\_PHAISEL

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 126259)

Hsing,Y.-I.C., Chow,T.-Y., Chen,C.-S., Wu,H.-P., Chao,Y.-T. and

Liu,S.-M.

Oryza sativa PAC P0496H07 genomic sequence

Unpublished

2 (bases 1 to 126259)

Hsing,Y.-I.C. and Chow,T.-Y.

Direct Submission

Submitted (14-AUG-2000) Institute of Botany, Academia Sinica, 128,

Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan

On Jun 23, 2001 this sequence version replaced gi:9800546.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 8 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 3786: contig of 3786 bp in length

\* 3787 3886: gap of unknown length

\* 3887 3886: contig of 4198 bp in length

\* 8085 8184: gap of unknown length

\* 8185 17489: contig of 9305 bp in length



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* 17490 17589; gap of unknown length
* 17590 33340: contig of 15751 bp in length
* 33341 33440: gap of unknown length
* 33441 45207: contig of 11767 bp in length
* 45208 45307: gap of unknown length
* 45308 56576: contig of 11269 bp in length
* 56577 92076: gap of unknown length
* 92077 92176: gap of unknown length
* 92177 126259: contig of 34083 bp in length.
FEATURES             Location/Qualifiers
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                        /db_xref="taxon:4530"
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BASE COUNT  34916 a 27527 c 27611 g 35499 t 706 others
ORIGIN
Query Match          4.3%; Score 19; DB 2; Length 126259;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy  90  GCGGTGGTGGCGATGGCG 108
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Db   6539 GCGGTGGTGGCGATGGCG 6557

RESULT 4
AC090441/c
LOCUS       AC090441      139468 bp    DNA    linear    PLN 12-FEB-2002
DEFINITION  Oryza sativa chromosome 10 clone OSJNB0052C09, complete sequence.
ACCESSION   AC090441
VERSION     AC090441.3  GI:15027729
KEYWORDS    HTG.
SOURCE      Oryza sativa.
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 139468)
            Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
            Saski, C., Henry, D., Oates, R. and Simmons, J.
            Rice Genomic Sequence
            Unpublished
REFERENCE   2 (bases 1 to 139468)
            Wing, R.A., Frisch, D., Presting, G., Wood, T., Yu, Y., Soderlund, C.,
            Kim, H.-R., Rambo, T., Henry, D. and Simmons, J.
            Direct Submission
            Submitted (23-FEB-2001) Clemson University Genomics Institute,
            Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE   3 (bases 1 to 139468)
            Wing, R.A., Frisch, D., Presting, G., Wood, T., Yu, Y., Soderlund, C.,
            Kim, H.-R., Rambo, T., Henry, D. and Simmons, J.
            Direct Submission
            Submitted (15-JUN-2001) Clemson University Genomics Institute,
            Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE   4 (bases 1 to 139468)
            Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
            Saski, C., Henry, D., Oates, R. and Simmons, J.
            Direct Submission
            Submitted (28-JUL-2001) Clemson University Genomics Institute,
            Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE   5 (bases 1 to 139468)
            Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
            Saski, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Mao, L.
            Direct Submission
            Submitted (15-AUG-2001) Clemson University Genomics Institute,
            Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE   6 (bases 1 to 139468)
            Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T.,
            Saski, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Sun, S.
            Direct Submission

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JOURNAL      Submitted (12-FEB-2002) Clemson University Genomics Institute,
              Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
COMMENT      On Jul 28, 2001 this sequence version replaced gi:14530842.
              This sequence was finished as follows unless otherwise noted: all
              regions were either double-stranded or sequenced with an alternate
              chemistry or covered by high quality data (i.e., phred quality
              >=30); an attempt was made to resolve all sequencing problems, such
              as compressions and repeats; all regions were covered by more than
              one plasmid subclone; and the assembly was confirmed by
              restriction digest. The assembly overlaps from base 120046-139468
              with OSJNB0045C13 (accession # AC079634). The overlap is from
              bases 1-19422 on OSJNB0045C13. On OSJNB0052C09 from base 30401
              to 30410 the consensus is below phred 30 even after multiple
              attempts to increase quality.
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                        AEDAGVAFVQPFREDGVDPDGYRANHRVFFDCTELGDLGQGITVYGCTCLPFRV
                        ALYGVDPFRRMSGGVGTADPAKFGESAPFLASVRAEOSHSDGDDGATAEASALVSLCA
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gene                gene
CDS                 CDS

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AP001111
ACCESSION
AP001111.1 GI:6863078
VERSION
KEYWORDS
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Oryza sativa DNA, clone:P0699E04.
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (sites)
Hsing,Y.C., Chow,T., Chen,C., Wu,H., Chu,M., Chao,Y. and Liu,S.
Oryza sativa PAC P0699E04 genomics sequence, complete sequence
Unpublished
2 (bases 1 to 175439)
Hsing,Y.C. and Chow,T.
Direct Submission
Submitted (28-JAN-2000) Yue-ie C. Hsing, Academia Sinica, Institute
of Botany; 218, Section 2, Yien-chu-yuan Road, Nankang, Taipei
11529, Taiwan (E-mail:bohsing@ccvax.sinica.edu.tw,
URL:http://biometrics.sinica.edu.tw/genome/,
Tel:886-2-27899590(ex.312), Fax:886-2-27827954)
The orientation of the sequence is from Sp6 to T7 of the PAC clone.
Genes were predicated from the integrated results of the
following: BLASTN2.0, BLASTX2.0, GENSCAN (Chris Burge,
http://gnomic.stanford.edu/
chris/GENSCANW.html), GRAIL (available by anonymous ftp from
arthur.epm.ornl.gov) and NetPlantGene
(http://www.cbs.dtu.dk/netgene/cbsnetgene.html). The sequence
was searched against the NCBI database.
FEATURES
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RESULT 6  
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LOCUS Xanthomonas axonopodis pv. citri str. 306, section 54 of 469 of  
the complete genome.  
DEFINITION AE011676 AE008923  
VERSION AE011676.1 GI:21106580  
KEYWORDS  
SOURCE Xanthomonas axonopodis pv. citri str. 306.  
ORGANISM Xanthomonas axonopodis pv. citri str. 306  
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
Xanthomonas

1 (bases 1 to 10144)  
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,  
Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida  
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,  
Camargo,L.E.A., Canarotte,G., Cannavan,F., Cardoso,J.,  
Chamberg,F., Clapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L.,  
Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,  
Ferreira,R.C.C., Ferro,M.T.F., Formighieri,E.F., Franco,M.C.,  
Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite  
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,  
Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,  
Mench,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,  
Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A.,  
Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,  
Takit,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos  
Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and  
Kitajima,J.P.

TITLE Comparison of the genomes of two Xanthomonas pathogens with  
differing host specificities  
JOURNAL Nature 417 (6887), 459-463 (2002)  
MEDLINE 22022145  
PUBMED 12024217

REFERENCE  
2 (bases 1 to 10144)  
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,  
Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida  
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,  
Camargo,L.E.A., Canarotte,G., Cannavan,F., Cardoso,J.,  
Chamberg,F., Clapina,L.P., Ciccarelli,R.M.B., Coutinho,L.L.,  
Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,  
Ferreira,R.C.C., Ferro,M.T.F., Formighieri,E.F., Franco,M.C.,  
Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite  
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,  
Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J.,  
Mench,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,  
Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A.,  
Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,  
Takit,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos  
Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and  
Kitajima,J.P.  
Direct Submission  
Submitted (28-NOV-2001) Departamento de Bioquimica, Universidade de  
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,  
Brazil

FEATURES  
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complete cds.  
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AF028006  
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Methanosarcina barkeri  
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
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REFERENCE  
1 (bases 1 to 10527)  
Sumi,M., Yoshida,M., Koga,Y. and Yoshida,M.  
F0P1-Artpase genes from an archaeobacterium, Methanosarcina barkeri  
Biochem. Biophys. Res. Commun. 241 (2), 427-433 (1997)  
98086367  
PUBMED  
2 (bases 1 to 10527)  
Sumi,M., Yoshida,M., Koga,Y. and Yoshida,M.  
Direct Submission  
Submitted (03-OCT-1997) The Research Laboratory for Resources  
Utilization, Tokyo Institute of Technology, 4259 Nagatsuta,  
Midori-ku, Yokohama, Kanagawa 226, Japan  
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TITLE Comparison of the genomes of two Xanthomonas pathogens with differing host specificities  
JOURNAL Nature 417 (6887), 459-463 (2002)  
MEDLINE 2202145  
PUBMED 12024217  
REFERENCE 2 (bases 1 to 10895)  
AUTHORS da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chamergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorriy, H., Faria, J.B., Ferreira, A.J.S., Ferris, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, D.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locati, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Secubal, J.C. and Kitajima, J.P.

TITLE Direct Submission  
JOURNAL Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900, Brazil

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AC014124  
VERSION AC014124.1 GI:6437211  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE Drosophila melanogaster.  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 36690)  
AUTHORS Adams,M. and Venter,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA  
COMMENT This sequence was identified as CDM:10213424 by the submitter.  
For further information on this sequence e-mail to fly@celera.com.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

FEATURES  
source  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 11  
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DEFINITION Homo sapiens chromosome 4 clone RP11-124H2 map 4, LOW-PASS SEQUENCE
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VERSION AC062001.1 GI:7630740
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ORGANISM Homo sapiens
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  2 (bases 1 to 82815)
    Birren, B., Linton, L., Nusbaum, C. and Lander, E.
    Homo sapiens chromosome 4, clone RP11-124H2
    Unpublished
  3 (bases 1 to 82815)
    Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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    Young, G., Zainoun, J., Zimmer, A. and Zody, M.
    Direct Submission
    Submitted (21-APR-2000) Whitehead Institute/MIT Center for Genome
    Research, 320 Charles Street, Cambridge, MA 02141, USA
    All repeats were identified using RepeatMasker:
    Smit, A.F.A. & Green, P. (1996-1997)
    http://ftp.genome.washington.edu/RM/RepeatMasker.html
    ----- Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence.submissions@genome.wi.mit.edu
    ----- Project Information
    Center project name: L9871
    Center clone name: 124_H_2
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    * NOTE: This record contains 78 individual
    * sequencing reads that have not been assembled into
    * contigs. Runs of N are used to separate the reads
    * and the order in which they appear is completely
    * arbitrary. Low-pass sequence sampling is useful for
    * identifying clones that may be gene-rich and allows
    * overlap relationships among clones to be deduced.
    * However, it should not be assumed that this clone
    * will be sequenced to completion. In the event that
    * the record is updated, the accession number will
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 ORGANISM Rhodobacter capsulatus  
 Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;

REFERENCE  
 AUTHORS Kumar,V., Fonstein,M. and Haselkorn,R.  
 TITLE Bacterium genome sequence  
 JOURNAL Nature 381 (6584), 653-654 (1996)  
 MEDLINE 96260014  
 PUBMED 8649508  
 REFERENCE  
 AUTHORS Fonstein,M., Kumar,V. and Haselkorn,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-1996) M. Fonstein, MGCB, Univ of Chicago, 920 E. 58th, Chicago, IL 60637, USA  
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 1 others

BASE COUNT 15089 a 28056 c 28787 g 14963 t  
 ORIGIN

Query Match 4.1%; Score 18; DB 1; Length 86896;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 AGCGTGGCGTCACGGC 75  
 Db 76328 AGCGTGGCGTCACGGC 76311  
 |||||

RESULT 13  
 AP003026/c  
 LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:RP11-21N9, complete sequence.  
 DEFINITION AP003026.2 GI:14861119  
 ACCESSION AP003026  
 VERSION AP003026.2  
 KEYWORDS HTG.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE Homo sapiens genomic DNA  
 JOURNAL Published Only in Database (2000)  
 REFERENCE  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gs.c.riken.go.jp, URL:http://hgp.gs.c.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  
 On Jul 17, 2001 this sequence version replaced gi:11611633.

BASE COUNT 32096 a 20123 c 20154 g 32429 t  
 ORIGIN

Query Match 4.1%; Score 18; DB 9; Length 104802;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 TATACCATTTTGTCAAGC 253  
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Db 31508 TATACATTTCCTCAAGC 31491

RESULT 14

LMFLCHR31\_13

WPCOMMENT

Sequence split into 22 fragments LOCUS LMFLCHR31 Accession AL499621

| Fragment Name | Begin   | End     |
|---------------|---------|---------|
| LMFLCHR31_00  | 1       | 110000  |
| LMFLCHR31_01  | 100001  | 210000  |
| LMFLCHR31_02  | 200001  | 310000  |
| LMFLCHR31_03  | 300001  | 410000  |
| LMFLCHR31_04  | 400001  | 510000  |
| LMFLCHR31_05  | 500001  | 610000  |
| LMFLCHR31_06  | 600001  | 710000  |
| LMFLCHR31_07  | 700001  | 810000  |
| LMFLCHR31_08  | 800001  | 910000  |
| LMFLCHR31_09  | 900001  | 1010000 |
| LMFLCHR31_10  | 1000001 | 1110000 |
| LMFLCHR31_11  | 1100001 | 1210000 |
| LMFLCHR31_12  | 1200001 | 1310000 |
| LMFLCHR31_13  | 1300001 | 1410000 |
| LMFLCHR31_14  | 1400001 | 1510000 |
| LMFLCHR31_15  | 1500001 | 1610000 |
| LMFLCHR31_16  | 1600001 | 1710000 |
| LMFLCHR31_17  | 1700001 | 1810000 |
| LMFLCHR31_18  | 1800001 | 1910000 |
| LMFLCHR31_19  | 1900001 | 2010000 |
| LMFLCHR31_20  | 2000001 | 2110000 |
| LMFLCHR31_21  | 2100001 | 2117963 |

Continuation (14 of 22) of LMFLCHR31 from base 1300001 (AL499621 Leishmania major chr

Query Match

Best Local Similarity 4.1%; Score 18; DB 2; Length 110000;

Mismatches 18; Conservative 0; Pred. No. 80;

Matches 18; Indels 0; Gaps 0;

QY 91 GCGGTGGTGGCGATGCG 108

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Db 38174 GCGGTGGTGGCGATGCG 38191

RESULT 15

LMFLCHR32\_21

WPCOMMENT

Sequence split into 28 fragments LOCUS LMFLCHR32 Accession AL499622

| Fragment Name | Begin   | End     |
|---------------|---------|---------|
| LMFLCHR32_00  | 1       | 110000  |
| LMFLCHR32_01  | 100001  | 210000  |
| LMFLCHR32_02  | 200001  | 310000  |
| LMFLCHR32_03  | 300001  | 410000  |
| LMFLCHR32_04  | 400001  | 510000  |
| LMFLCHR32_05  | 500001  | 610000  |
| LMFLCHR32_06  | 600001  | 710000  |
| LMFLCHR32_07  | 700001  | 810000  |
| LMFLCHR32_08  | 800001  | 910000  |
| LMFLCHR32_09  | 900001  | 1010000 |
| LMFLCHR32_10  | 1000001 | 1110000 |
| LMFLCHR32_11  | 1100001 | 1210000 |
| LMFLCHR32_12  | 1200001 | 1310000 |
| LMFLCHR32_13  | 1300001 | 1410000 |
| LMFLCHR32_14  | 1400001 | 1510000 |
| LMFLCHR32_15  | 1500001 | 1610000 |
| LMFLCHR32_16  | 1600001 | 1710000 |
| LMFLCHR32_17  | 1700001 | 1810000 |
| LMFLCHR32_18  | 1800001 | 1910000 |
| LMFLCHR32_19  | 1900001 | 2010000 |
| LMFLCHR32_20  | 2000001 | 2110000 |
| LMFLCHR32_21  | 2100001 | 2210000 |
| LMFLCHR32_22  | 2200001 | 2310000 |
| LMFLCHR32_23  | 2300001 | 2410000 |
| LMFLCHR32_24  | 2400001 | 2510000 |
| LMFLCHR32_25  | 2500001 | 2610000 |
| LMFLCHR32_26  | 2600001 | 2710000 |



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| PR | 19-APR-1999; | 99US-0130077. | PR | 19-JUL-1999; | 99US-0144335. |
| PR | 21-APR-1999; | 99US-0130449. | PR | 20-JUL-1999; | 99US-0144352. |
| PR | 23-APR-1999; | 99US-0130510. | PR | 20-JUL-1999; | 99US-0144632. |
| PR | 28-APR-1999; | 99US-0130891. | PR | 20-JUL-1999; | 99US-0144684. |
| PR | 23-APR-1999; | 99US-0131449. | PR | 21-JUL-1999; | 99US-0144814. |
| PR | 30-APR-1999; | 99US-0132047. | PR | 21-JUL-1999; | 99US-0145086. |
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| PR | 04-MAY-1999; | 99US-0132484. | PR | 22-JUL-1999; | 99US-0145085. |
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| PR | 06-MAY-1999; | 99US-0132487. | PR | 22-JUL-1999; | 99US-0145192. |
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| PR | 09-JUL-1999; | 99US-0142920. | PR | 24-SEP-1999; | 99US-0155659. |
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Query Match 7.7%; Score 34; DB 21; Length 462;

Best Local Similarity 100.0%; Pred. No. 1.1e-08; Mismatches 0; Indels 0; Gaps 0;

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Qy 20 CGCCTTTTCGTCGCCGTCAGCGTCGCCGCTCC 53

Db 61 CGCCTTTTCGTCGCCGTCAGCGTCGCCGCTCC 94

#### RESULT 2

AAC43563  
ID AAC43563 standard; DNA; 405 BP.

XX AC AAC43563;

XX DT 17-OCT-2000 (first entry)

XX DE Zea mays DNA fragment SEQ ID NO: 39686.

XX KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

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PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
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PR 13-OCT-1999; 99US-0159298.  
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PR 25-OCT-1999; 99US-0161404.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 5.9%; Score 26; DB 21; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0.00028;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 AGGCAGCGGTGGTGGCGATGGCGT 109  
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Db 106 AGGCAGCGGTGGTGGCGATGGCGT 131

## RESULT 3

AAC51740

ID AAC51740 standard: DNA; 455 BP.

XX AC AAC51740;

XX DT 18-OCT-2000 (first entry)

XX DE Zea mays DNA fragment SEQ ID NO: 69614.

XX KW Hybridisation assay; genetic mapping; gene expression control;

XX KW protein identification; signal transduction pathway; metabolic;

XX KW pathway; promoter; termination sequence; corn; ss.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

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XX PR 28-APR-1999; 99US-0130891.

XX PR 30-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 04-MAY-1999; 99US-0132407.

XX PR 05-MAY-1999; 99US-0132484.

XX PR 06-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 07-MAY-1999; 99US-0132487.

XX PR 11-MAY-1999; 99US-0132863.

XX PR 14-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.



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PR 16-JUL-1999; 99US-0144086.  
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PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
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PR 04-OCT-1999; 99US-0157117.  
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PR 22-OCT-1999; 99US-0160989.

PR 25-OCT-1999; 99US-0161404.  
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PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 4.5%; Score 20; DB 21; Length 455;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCCTTTTCGTCGCCGCGTC 39  
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DB 84 CGCCTTTTCGTCGCCGCGTC 103  
|||||

RESULT 4  
AAZ52325  
ID AAZ52325 standard; DNA; 1503 BP.  
XX  
AC AAZ52325;  
XX  
DT 24-JUL-2000 (first entry)  
XX  
DE Klebsiella oxytoca LyxK gene.  
XX  
KW LyxK-S operon; LyxK; YiaJ; regulatory sequence; YiaK; YiaL; ORF1; YiaX2;  
KW YiaR; YiaS; carbohydrate utilisation; screening; metabolic pathway;  
KW biological synthesis; anti-infective; antibacterial; ds.  
XX  
OS Klebsiella oxytoca.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1503  
FT /tag= a  
FT /product= "Klebsiella oxytoca LyxK protein"  
FT /note= "Does not include stop codon"  
FT /partial  
XX  
XX WO200022170-A1.  
XX  
XX 20-APR-2000.  
XX  
XX 12-OCT-1999; 99WO-US23862.  
XX  
XX 14-OCT-1998; 98US-0172952.  
XX (MICR-) MICROGENOMICS INC.  
XX  
XX Hoch J, Dartois V;  
XX  
XX WPI; 2000-318013/27.  
XX P-PSDB; AAY70727.  
XX  
XX Screening for metabolic pathways, useful to provide for the biological  
XX production of chemicals, antibacterials and other anti-infectives,  
XX using cells which provide a signal in the presence of a compound  
XX produced by the pathway.  
XX  
XX Claim 40a; Page 98-99; 137pp; English.  
XX  
XX The present DNA sequence is the Klebsiella oxytoca LyxK gene, of the  
XX LyxK-S operon. It includes the genes encoding the via operon-related  
XX polypeptides, YiaK, YiaL, ORF1, YiaX2, YiaQ, YiaR and YiaS. It is  
XX preceded by the transcriptional regulatory sequence YiaJ. The function  
XX of the Yia operon gene products are unknown. It is homologous to YiaK-S  
XX operon of Escherichia coli and Haemophilus influenzae, which may be  
XX involved in carbohydrate utilisation. The E.coli LyxK encoded enzyme  
XX phosphorylates L-xylulose and plays an important role in the utilisation

CC of L-xylulose by E.coli. This operon is used in a method for screening  
CC nucleotide sequences, the products of which can convert a source compound  
CC to a target compound, using cells which can provide a detectable signal  
CC in the presence of the target compound. This sequence is used to screen  
CC and identify biological pathways, that can be used for the biological  
CC synthesis of chemicals, antibacterials and other anti-infectives.  
XX  
SQ Sequence 1503 BP; 287 A; 463 C; 456 G; 297 T; 0 other;  
Query Match 3.9%; Score 17; DB 21; Length 1503;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 TCGCGGTGTCACCGCGGC 78  
|||||  
DB 1199 TCGCGGTGTCACCGCGGC 1215  
|||||

RESULT 5  
ABL18169/C  
ID ABL18169 standard; DNA; 2219 BP.  
XX  
AC ABL18169;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5980.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ds.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
XX  
XX 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Claim 1; SEQ ID NO 5980; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (AB857737-AB872072).  
XX  
XX The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2219 BP; 523 A; 673 C; 579 G; 444 T; 0 other;  
Query Match 3.9%; Score 17; DB 23; Length 2219;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGTGTCGATGCGC 108

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Db      801 CGGTGGTGGCGATGGCG 785
|||||
RESULT 6
ABL14523/C
ID      ABL14523 standard; cDNA; 2487 BP.
XX
AC      ABL14523;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster expressed polynucleotide SEQ ID NO 38051.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ss.
XX
OS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US09231.
XX
PR      23-MAR-2000; 2000US-191637P.
XX
PT      11-JUL-2000; 2000US-0614150.
XX
PA      (PEKE ) PE CORP NY.
XX
PI      Venter JC, Adams M, Li PWD, Myers EW;
XX
DR      WPI; 2001-656860/75.
XX
P-PSDB; ABB70420.
XX
PT      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX
XX
Claim 1; SEQ ID NO 38051; 21pp + Sequence Listing; English.
XX
CC      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins
CC      (ABB57737-ABB72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ      Sequence 2487 BP; 608 A; 737 C; 639 G; 503 T; 0 other;

Query Match          3.9%; Score 17; DB 23; Length 2487;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      92 CGGTGGTGGCGATGGCG 108
|||||
DB      1069 CGGTGGTGGCGATGGCG 1053

RESULT 7
AAH67505
ID      AAH67505 standard; DNA; 2844 BP.
XX
AC      AAH67505;
XX
DT      26-SEP-2001 (first entry)
XX
DE      C glutamicum coding sequence fragment SEQ ID NO: 2540.

```

```

XX      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW      organic acid synthesis; ds.
XX
OS      Corynebacterium glutamicum.
XX
PN      EPI108790-A2.
XX
PD      20-JUN-2001.
XX
PF      18-DEC-2000; 2000EP-0127688.
XX
PR      16-DEC-1999; 99JP-0377484.
XX
PR      07-APR-2000; 2000JP-0159162.
XX
PR      03-AUG-2000; 2000JP-0280988.
XX
PA      (AYOW ) KYOWA HAKKO KOGYO KK.
XX
XX      Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX      Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX      WPI; 2001-376931/40.
XX      P-PSDB; AAG92286.
XX
PT      Novel polynucleotides derived from Coryneform bacteria, for identifying
PT      mutation point of a gene, measuring expression of a gene, analysing
PT      expression profile or pattern of a gene and identifying homologous gene
PT      -
XX
XX      Claim 8; SEQ ID NO: 2540; 246pp + Sequence Listing; English.
XX
CC      The present invention provides a number of nucleotide and protein
CC      sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC      are useful for identifying the mutation point of a gene derived from a
CC      mutant of coryneform bacterium, measuring expression amount and
CC      analysing the expression profile or expression pattern of a gene derived
CC      from Coryneform bacterium, and identifying a homologue of a gene derived
CC      from coryneform bacterium. Coryneform bacteria are useful for producing
CC      amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC      particularly L-lysine. The present sequence is a nucleic acid described
CC      in the exemplification of the invention.
CC      Note: The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from the
CC      European Patent Office.
XX
SQ      Sequence 2844 BP; 676 A; 786 C; 760 G; 622 T; 0 other;

Query Match          3.9%; Score 17; DB 22; Length 2844;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CGCGGCGCGACTTCGCC 23
|||||
DB      1896 CGCGGCGCGACTTCGCC 1912

RESULT 8
AAF71426
ID      AAF71426 standard; DNA; 2858 BP.
XX
AC      AAF71426;
XX
DT      30-APR-2001 (first entry)
XX
DE      Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:133.
XX
XX      Corynebacterium glutamicum; carbon metabolism and energy production;
KW      SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW      fine chemical production; organic acid; proteinogenic amino acid;
KW      nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW      nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW      carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW      diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.

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XX OS Corynebacterium glutamicum.  
XX WO200100844-A2.  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-IB00943.  
XX PR 25-JUN-1999; 99US-0141031.  
PR 08-JUL-1999; 99DE-1031412.  
PR 08-JUL-1999; 99DE-1031413.  
PR 08-JUL-1999; 99DE-1031419.  
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PR 08-JUL-1999; 99DE-1031562.  
PR 08-JUL-1999; 99DE-1031634.  
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PR 08-JUL-1999; 99DE-1032227.  
PR 08-JUL-1999; 99DE-1032230.  
PR 08-JUL-1999; 99US-0143208.  
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PR 14-JUL-1999; 99DE-1032973.  
PR 14-JUL-1999; 99DE-1033005.  
PR 27-AUG-1999; 99DE-1040765.  
PR 31-AUG-1999; 99US-0151572.  
PR 03-SEP-1999; 99DE-1042076.  
PR 03-SEP-1999; 99DE-1042079.  
PR 03-SEP-1999; 99DE-1042086.  
PR 03-SEP-1999; 99DE-1042087.  
PR 03-SEP-1999; 99DE-1042088.  
PR 03-SEP-1999; 99DE-1042095.  
PR 03-SEP-1999; 99DE-1042123.  
PR 03-SEP-1999; 99DE-1042125.  
XX PA (BADI ) BASE AG.  
XX PI Pompejus M, Kroeger B, Schroeder H, Zeider O, Haberhauer G;  
XX DR WPI; 2001-061975/07.  
XX DR P-PSDB; AAB79309.  
XX PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
PT metabolism and oxidative phosphorylation protein for production or  
PT modulation of production of fine chemicals e.g. amino acids,  
PT carbohydrates or enzymes -  
XX PS Claim 3; Page 342-345; 1246pp; English.  
XX CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
CC metabolism and oxidative phosphorylation (SMP) proteins given in  
CC AAB79243 to AAB 79633 which are involved in carbon metabolism and  
CC energy production. The C. glutamicum SMP gene can be used in vectors  
CC (ii) for expression in host cells and production or modulation of  
CC production of fine chemicals, such as, an organic acid, a proteinogenic  
CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,  
CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty  
CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a  
CC cofactor, a polypeptide, or an enzyme. The presence of (i) or SMP proteins  
CC (iii) encoded by them are used for diagnosing the presence or activity of  
CC Corynebacterium diptheriae in a subject. (i), (ii), (iii) or host cells  
CC containing them are used to map genomes of organisms related to  
CC C. glutamicum, identify and localise C. glutamicum sequences of interest,  
CC in evolutionary studies, in determining SMP protein regions required  
CC for function, in modulating SMP protein activity, in modulating the  
CC metabolism of sugars, and in modulating high-energy molecule production  
CC in a cell (i.e. ATP, NADPH).  
XX

XX SQ Sequence 2858 BP; 680 A; 789 C; 764 G; 625 T; 0 other;  
XX Query Match 3.9%; Score 17; DB 23; Length 2858;  
XX Best Local Similarity 100.0%; Pred. No. 26;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CGCGGCGGCGACTTGGCC 23  
DB 1887 CGCGGCGGCGACTTGGCC 1903  
RESULT 9  
ABL18381/c  
ID ABL18381 standard; DNA; 2957 BP.  
XX AC ABL18381;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6616.  
XX KW Drosophila; developmental biology; cell signalling; insecticide;  
XX KW pharmaceutical; gene; ds.  
XX OS Drosophila melanogaster.  
XX WO200171042-A2.  
XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US09231.  
XX PR 23-MAR-2000; 2000US-191637P.  
XX PR 11-JUL-2000; 2000US-0614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions -  
XX PS Claim 1; SEQ ID NO 6616; 21pp + Sequence Listing; English.  
XX CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (AAB57737-ABR72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_sequences.  
XX SQ Sequence 2957 BP; 717 A; 845 C; 736 G; 659 T; 0 other;  
XX Query Match 3.9%; Score 17; DB 23; Length 2957;  
XX Best Local Similarity 100.0%; Pred. No. 26;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 92 CGGTGGTGGCGATGCG 108  
DB 1539 CGGTGGTGGCGATGCG 1523  
RESULT 10  
AAF71425  
ID AAF71425 standard; DNA; 2967 BP.

XX AAF71425;  
 CC 30-APR-2001 (first entry)  
 CC Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:131.  
 CC  
 CC Corynebacterium glutamicum; carbon metabolism and energy production;  
 CC SMP protein; sugar metabolism; organic acid; oxidative phosphorylation protein;  
 CC fine chemical production; organic acid; proteinogenic amino acid;  
 CC nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 CC nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 CC carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 CC diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.  
 CC  
 CC Corynebacterium glutamicum.  
 CC  
 CC WO200100844-A2.  
 CC  
 CC 04-JAN-2001.  
 CC  
 CC 23-JUN-2000; 2000WO-IB00943.  
 CC  
 CC 25-JUN-1999; 99US-0141031.  
 CC 08-JUL-1999; 99DE-1031412.  
 CC 08-JUL-1999; 99DE-1031413.  
 CC 08-JUL-1999; 99DE-1031419.  
 CC 08-JUL-1999; 99DE-1031420.  
 CC 08-JUL-1999; 99DE-1031424.  
 CC 08-JUL-1999; 99DE-1031428.  
 CC 08-JUL-1999; 99DE-1031431.  
 CC 08-JUL-1999; 99DE-1031433.  
 CC 08-JUL-1999; 99DE-1031434.  
 CC 08-JUL-1999; 99DE-1031510.  
 CC 08-JUL-1999; 99DE-1031562.  
 CC 08-JUL-1999; 99DE-1031634.  
 CC 08-JUL-1999; 99DE-1032180.  
 CC 09-JUL-1999; 99DE-1032227.  
 CC 09-JUL-1999; 99DE-1032230.  
 CC 09-JUL-1999; 99US-0143208.  
 CC 14-JUL-1999; 99DE-1032924.  
 CC 14-JUL-1999; 99DE-1032973.  
 CC 14-JUL-1999; 99DE-1033005.  
 CC 27-AUG-1999; 99DE-1040765.  
 CC 31-AUG-1999; 99US-0151572.  
 CC 03-SEP-1999; 99DE-1042076.  
 CC 03-SEP-1999; 99DE-1042079.  
 CC 03-SEP-1999; 99DE-1042086.  
 CC 03-SEP-1999; 99DE-1042087.  
 CC 03-SEP-1999; 99DE-1042088.  
 CC 03-SEP-1999; 99DE-1042095.  
 CC 03-SEP-1999; 99DE-1042123.  
 CC 03-SEP-1999; 99DE-1042125.  
 CC  
 CC (BADI ) BASF AG.  
 CC  
 CC Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
 CC  
 CC WPI: 2001-061975/07.  
 CC P-PSDB; AAB79308.  
 CC  
 CC New Isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
 CC metabolism and oxidative phosphorylation protein for production or  
 CC modulation of production of fine chemicals e.g. amino acids,  
 CC carbohydrates or enzymes -  
 CC  
 CC Claim 3; Page 334-338; 1246pp; English.  
 CC  
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
 CC metabolism and oxidative phosphorylation (SMP) proteins given in  
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and  
 CC energy production. The C. glutamicum SMP gene can be used in vectors  
 CC (ii) for expression in host cells and production or modulation of

CC production of fine chemicals, such as, an organic acid, a proteinogenic  
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,  
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty  
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a  
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins  
 CC (iii) encoded by them are used for diagnosing the presence or activity of  
 CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells  
 CC containing them are used to map genomes of organisms related to  
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,  
 CC in evolutionary studies, in determining SMP protein regions required  
 CC for function, in modulating SMP protein activity, in modulating the  
 CC metabolism of sugars, and in modulating high-energy molecule production  
 CC in a cell (i.e. ATP, NADPH).  
 CC  
 CC Sequence 2967 BP; 712 A; 819 C; 782 G; 654 T; 0 other;  
 CC  
 CC Query Match 3.9%; Score 17; DB 22; Length 2967;  
 CC Best Local Similarity 100.0%; Pred. No. 26;  
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 7 CGCCGGCGGACTTCGCC 23  
 CC |||||  
 CC Db 1996 CGCCGGCGGACTTCGCC 2012  
 CC  
 CC RESULT 11  
 CC AAC76210  
 CC ID AAC76210 standard; cDNA; 3026 BP.  
 CC  
 CC AAC76210;  
 CC  
 CC 08-FEB-2001 (first entry)  
 CC  
 CC Human ORFX ORF1765 polynucleotide sequence SEQ ID NO:3529.  
 CC  
 CC Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 CC vulnary; antipruritic; antiparkinsonian; nootropic; neuroprotective;  
 CC anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 CC immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 CC hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 CC antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 CC antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 CC neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 CC cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 CC cholesterol ester storage; systemic lupus erythematosus; infection;  
 CC severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 CC allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 CC bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 CC thrombosis; contraceptive; ss.  
 CC  
 CC Homo sapiens.  
 CC  
 CC XX WO200058473-A2.  
 CC  
 CC 05-OCT-2000.  
 CC  
 CC 31-MAR-2000; 2000WO-US08621.  
 CC  
 CC 31-MAR-1999; 99US-0127607.  
 CC 02-APR-1999; 99US-0127636.  
 CC 03-APR-1999; 99US-0127728.  
 CC 30-MAR-2000; 2000US-0540763.  
 CC  
 CC (CURA-) CURAGEN CORP.  
 CC  
 CC Shimkets RA, Leach M;  
 CC  
 CC WPI: 2000-602362/57.  
 CC P-PSDB; AAB42001.  
 CC  
 CC Novel nucleic acids and peptides derived from open reading frame X,  
 CC useful for treating e.g. cancers, proliferative disorders,  
 CC neurodegenerative disorders and cardiovascular disease -  
 CC PT

XX Claim 5; Page 2695-2697; 5507pp; English.  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
CC antiparasitic; antiparkinsonian; nontropic; neuroprotective;  
CC osteopathic; anticonvulsant; antithyroid; immunosuppressive;  
CC immunostimulant; cardiast; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
CC antithyroid; and antianemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.  
XX Sequence 3026 BP; 619 A; 838 C; 955 G; 613 T; 1 other;  
SQ

Query Match 3.9%; Score 17; DB 21; Length 3026;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGCGACGGCGGTGTGCG 101  
|||||  
DB 767 GGCGACGGCGGTGTGCG 783

RESULT 12  
AAK80242/c  
ID AAK80242 standard; DNA; 5282 BP.  
AC AAK80242:  
XX  
XX  
XX 07-NOV-2001 (first entry)  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35054.  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX Homo sapiens.  
XX WO200157182-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01354.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190070.  
XX 18-APR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0205515.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 11-JUL-2000; 2000US-0217496.  
XX 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225287.  
PR 14-AUG-2000; 2000US-0225288.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228934.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231988.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 25-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241828.  
PR 01-NOV-2000; 2000US-0244617.  
PR 09-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 17-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251889.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and  
XX metastasis -  
XX  
XX  
XX  
XX  
XX Disclosure; SEQ ID NO 35054; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
XX activity, and can be used in gene therapy and vaccine production. (I)  
XX proteins and polynucleotides may be used in the prevention, diagnosis and  
XX treatment of diseases associated with inappropriate (I) expression. For  
XX example, they may be used to treat disorders associated with decreased  
XX expression by rectifying mutations or deletions in a patient's genome  
XX that affect the activity of (I) by expressing inactive proteins or to  
XX supplement the patient's own production of (I). Additionally, (I)  
XX polynucleotides may be used to produce the secreted (I), by inserting  
XX the nucleic acids into a host cell and culturing the cell to express the  
XX protein. (I) proteins and polynucleotides may be used to prevent,  
XX diagnose and treat immune/hematopoietic-related diseases, especially

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 5282 BP; 1056 A; 1493 C; 1310 G; 1423 T; 0 other;  
Query Match 3.9%; Score 17; DB 22; Length 5282;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 286 AGGAGTTAAAGCTAGAG 302  
Db 622 AGGAGTTAAAGCTAGAG 606  
|||||  
RESULT 13  
ABLI8380  
ID ABLI8380 standard; DNA; 5437 BP.  
XX  
XX ABLI8380;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 6613.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmacological; gene; ds.  
XX  
XX Drosophila melanogaster.  
XX  
XX WC200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
XX  
XX 23-MAR-2000; 2000US-191637P.  
XX  
XX 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li FWD, Myers EW;  
XX  
XX WPI; 2001-856860/75.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions -  
XX  
XX Claim 1; SEQ ID NO 6613; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (ABLI6176-ABLI3051), expressed DNA  
XX sequences (ABLI01840-ABLI6175) and the encoded proteins  
XX (ABBS7737-ABBS72072).  
XX  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 5437 BP; 1371 A; 1260 C; 1381 G; 1425 T; 0 other;  
Query Match 3.9%; Score 17; DB 23; Length 5437;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 92 CGGTGGTGGCGATGGCG 108  
Db 2707 CGGTGGTGGCGATGGCG 2723  
|||||

```
RESULT 14
ABL14522
ID ABL14522 standard; cDNA; 5440 BP.
XX
AC ABL14522:
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38048.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PF 27-SEP-2001.
XX
PR 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
PI WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 5977; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABB72072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5440 BP; 1371 A; 1261 C; 1382 G; 1426 T; 0 other;

Query Match 3.9%; Score 17; DB 23; Length 5440;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGGTGGCGATGGCG 108
Db 2707 CGGTGGTGGCGATGGCG 2723

RESULT 15
ABL18168
ID ABL18168 standard; DNA; 5440 BP.
XX
AC ABL18168:
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5977.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
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KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
PI WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 5977; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABB72072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5440 BP; 1371 A; 1261 C; 1382 G; 1426 T; 0 other;

Query Match 3.9%; Score 17; DB 23; Length 5440;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGGTGGTGGCGATGGCG 108
Db 2707 CGGTGGTGGCGATGGCG 2723

Search completed: November 30, 2002, 02:40:01
Job time : 298 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 01:33:22 ; Search time 52 Seconds

(without alignments)  
2594.957 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgacttc.....gggaatnntagataaaaaa 440

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued\_Patents\_NA: \*

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2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2.6/ptodata/1/ina/PTCUS\_COMB.seq: \*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 17    | 3.9         | 1503   | 4  | US-09-172-952-6    |
| 2          | 17    | 3.9         | 9334   | 4  | US-09-172-952-19   |
| 3          | 16    | 3.6         | 286    | 4  | US-08-991-789A-17  |
| 4          | 16    | 3.6         | 286    | 4  | US-08-991-789A-292 |
| 5          | 16    | 3.6         | 286    | 4  | US-09-062-451-17   |
| 6          | 16    | 3.6         | 286    | 4  | US-09-598-326-17   |
| 7          | 16    | 3.6         | 393    | 4  | US-09-280-116-34   |
| 8          | 16    | 3.6         | 864    | 2  | US-08-901-306-1    |
| 9          | 16    | 3.6         | 864    | 4  | US-09-180-271-1    |
| 10         | 16    | 3.6         | 1569   | 2  | US-08-901-306-3    |
| 11         | 16    | 3.6         | 1569   | 4  | US-09-180-271-3    |
| 12         | 16    | 3.6         | 1998   | 4  | US-09-382-106-1    |
| 13         | 15    | 3.4         | 439    | 4  | US-09-222-575-149  |
| 14         | 15    | 3.4         | 576    | 1  | US-08-086-428B-38  |
| 15         | 15    | 3.4         | 576    | 2  | US-08-468-570-38   |
| 16         | 15    | 3.4         | 576    | 2  | US-08-290-665A-38  |
| 17         | 15    | 3.4         | 576    | 5  | PCF-US95-10398-38  |
| 18         | 15    | 3.4         | 610    | 4  | US-09-072-596-293  |
| 19         | 15    | 3.4         | 702    | 3  | US-09-094-148-1    |
| 20         | 15    | 3.4         | 715    | 4  | US-08-998-416-648  |
| 21         | 15    | 3.4         | 750    | 3  | US-09-167-717-3    |
| 22         | 15    | 3.4         | 767    | 1  | US-08-139-909-1    |
| 23         | 15    | 3.4         | 767    | 2  | US-08-308-821A-1   |
| 24         | 15    | 3.4         | 767    | 3  | US-08-831-627-1    |
| 25         | 15    | 3.4         | 796    | 4  | US-08-998-416-475  |
| 26         | 15    | 3.4         | 1010   | 2  | US-08-827-190-8    |
| 27         | 15    | 3.4         | 1010   | 4  | US-09-170-187-8    |

c 28 15 3.4 1362 4 US-08-818-112-7 Sequence 7, Appli  
c 29 15 3.4 1362 4 US-08-818-111-7 Sequence 7, Appli  
c 30 15 3.4 1362 4 US-09-056-556-7 Sequence 7, Appli  
c 31 15 3.4 1362 4 US-09-072-596-7 Sequence 7, Appli  
c 32 15 3.4 1932 4 US-09-171-699-7 Sequence 7, Appli  
c 33 15 3.4 1971 6 5349058-1 Patent No. 5349058  
c 34 15 3.4 2943 1 US-08-042-747A-7 Sequence 7, Appli  
c 35 15 3.4 2985 3 US-08-744-814-18 Sequence 18, Appli  
c 36 15 3.4 3217 4 US-09-232-200-64 Sequence 64, Appli  
c 37 15 3.4 3217 4 US-09-232-197-64 Sequence 64, Appli  
c 38 15 3.4 3217 4 US-09-232-201-64 Sequence 64, Appli  
c 39 15 3.4 3267 4 US-08-453-702B-170 Sequence 170, Appli  
c 40 15 3.4 3342 2 US-08-254-989-1 Sequence 1, Appli  
c 41 15 3.4 3645 2 US-08-663-112-1 Sequence 1, Appli  
c 42 15 3.4 11481 4 US-09-453-702B-254 Sequence 254, Appli  
c 43 15 3.4 11601 2 US-08-222-617A-3 Sequence 3, Appli  
c 44 15 3.4 11601 2 US-08-222-617A-24 Sequence 24, Appli  
c 45 15 3.4 34063 4 US-09-453-702B-96 Sequence 96, Appli

## ALIGNMENTS

RESULT 1  
US-09-172-952-6  
; Sequence 6, Application US/09172952  
; Patent No. 6368793  
; GENERAL INFORMATION:  
; APPLICANT: Hoch, James  
; APPLICANT: Dartois, Veronique  
; TITLE OF INVENTION: METABOLIC SELECTION METHODS  
; FILE REFERENCE: 234/191  
; CURRENT APPLICATION NUMBER: US/09/172,952  
; CURRENT FILING DATE: 1998-10-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 1503  
; TYPE: DNA  
; ORGANISM: lyxk  
US-09-172-952-6

Query Match 3.9%; Score 17; DB 4; Length 1503;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 TCGCGCTCACCGCGGC 78  
DB 1199 TCGCGCTCACCGCGGC 1215  
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RESULT 2  
US-09-172-952-19  
; Sequence 19, Application US/09172952  
; Patent No. 6368793  
; GENERAL INFORMATION:  
; APPLICANT: Hoch, James  
; APPLICANT: Dartois, Veronique  
; TITLE OF INVENTION: METABOLIC SELECTION METHODS  
; FILE REFERENCE: 234/191  
; CURRENT APPLICATION NUMBER: US/09/172,952  
; CURRENT FILING DATE: 1998-10-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 9334  
; TYPE: DNA  
; ORGANISM: yia  
US-09-172-952-19

Query Match 3.9%; Score 17; DB 4; Length 9334;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 TGCCTCACCCTGGCG 78  
Db 6414 TGCCTCACCCTGGCG 6430  
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RESULT 3  
US-08-991-789A-17  
; Sequence 17, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,789A  
; FILING DATE: 11-Dec-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-08-991-789A-17

Query Match 3.6%; Score 16; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTGGTGGCGATGGCG 108  
Db 172 GGTGGTGGCGATGGCG 187  
/TTTTTTTTTTTTTTTT/

RESULT 4  
US-08-991-789A-292  
; Sequence 292, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle

; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,789A  
; FILING DATE: 11-Dec-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 292:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 292:  
US-08-991-789A-292

Query Match 3.6%; Score 16; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTGGTGGCGATGGCG 108  
Db 172 GGTGGTGGCGATGGCG 187  
/TTTTTTTTTTTTTTTT/

RESULT 5  
US-09-062-451-17  
; Sequence 17, Application US/09062451  
; Patent No. 6344550  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 297  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/062,451  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-062-451-17

Query Match          3.6%; Score 16; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGCG 108
    |||
DB 172 GGTGGTGGCGATGCG 187

RESULT 6
US-09-598-326-17
; Sequence 17, Application US/09598326
; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
;              Smith, John M.
;              Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                   TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 247
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/598,326
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-598-326-17

Query Match          3.6%; Score 16; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGCG 108
    |||
DB 172 GGTGGTGGCGATGCG 187

RESULT 7
US-09-280-116-34
; Sequence 34, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
```

```
;
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aspartyl proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(393)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-34

Query Match          3.6%; Score 16; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCGCGCGCGCGCA 16
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DB 6 CGTCGCGCGCGCGCA 21

RESULT 8
US-08-901-306-1
; Sequence 1, Application US/08901306
; Patent No. 5955319
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: BREME, Umberto
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: LOMOVSKAYA, Natasha
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: OTTEN, Sharee
; APPLICANT: HUTCHINSON, Charles R.
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; FILE REFERENCE: 1615-7003
; CURRENT APPLICATION NUMBER: US/08/901,306
; CURRENT FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Streptomyces peucetius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(864)
US-08-901-306-1

Query Match          3.6%; Score 16; DB 2; Length 864;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCGCGCGCGCGCA 16
    |||
DB 719 CGTCGCGCGCGCGCA 734

RESULT 9
US-09-180-271-1
; Sequence 1, Application US/09180271
; Patent No. 6210930
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: LOMOVSKAYA, Natalia
; APPLICANT: FONSTEIN, Leonid
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: HUTCHINSON, C. Richard
```

```
; APPLICANT: OTTEN, Sharee L.
; APPLICANT: BREME, Umberto
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,271
; FILING DATE: 14-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03938
; FILING DATE: 05-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,306
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,412
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P1615-8010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..861
US-09-180-271-1
Query Match 3.6%; Score 16; DB 4; Length 864;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGCGCGCGCGCA 16
| | | | | | | | | | | | | | | |
Db 719 CGTCCGCGCGCGCGCA 734

RESULT 10
US-08-901-306-3
; Sequence 3, Application US/08901306
; Patent No. 5955319
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: BREME, Umberto
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: LOMOVSKAYA, Natasha
; APPLICANT: FORNSTEIN, Leonid
; APPLICANT: OTTEN, Sharee
; APPLICANT: HUTCHINSON, Charles R.
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; FILE REFERENCE: 1615-7003
; CURRENT APPLICATION NUMBER: US/08/901,306
; CURRENT FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Streptomyces peucetius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(255)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1219)..(1569)
US-08-901-306-3
Query Match 3.6%; Score 16; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGCGCGCGCGCA 16
| | | | | | | | | | | | | | | |
Db 970 CGTCCGCGCGCGCGCA 985

RESULT 11
US-09-180-271-3
; Sequence 3, Application US/09180271
; Patent No. 6210930
; GENERAL INFORMATION:
; APPLICANT: FILIPPINI, Silvia
; APPLICANT: LOMOVSKAYA, Natalia
; APPLICANT: FORNSTEIN, Leonid
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: HUTCHINSON, C. Richard
; APPLICANT: OTTEN, Sharee L.
; APPLICANT: BREME, Umberto
; TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,271
; FILING DATE: 14-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03938
; FILING DATE: 05-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,306
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/812,412
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P1615-8010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA
US-09-180-271-3

Query Match          3.6%; Score 16; DB 4; Length 1569;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCGCGCGCGCGCGA 16
    |||||||
Db 970 CGTCGCGCGCGCGCGA 985

RESULT 12
US-09-382-106-1
; Sequence 1, Application US/09382106
; Patent No. 6221631
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: Jiang, Xinhe
; APPLICANT: Mcdevitt, Damien
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: tkTA
; FILE REFERENCE: GM10236
; CURRENT APPLICATION NUMBER: US/09/382,106
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

Query Match          3.6%; Score 16; DB 4; Length 1998;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGGCGCGACTTCGCC 23
    |||||||
Db 996 GCGGCGCGACTTCGCC 1011

RESULT 13
US-09-222-575-149
; Sequence 149, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (359)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (384)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
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; LOCATION: (402)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-222-575-149

Query Match          3.4%; Score 15; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCGACTTCGCCTTTT 27
    |||||||
Db 226 CCGACTTCGCCTTTT 240

RESULT 14
US-08-086-428B-38
; Sequence 38, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homopapiens
; INDIVIDUAL ISOLATE: S52
US-08-086-428B-38

Query Match          3.4%; Score 15; DB 1; Length 576;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 ATGTTTCAGGACATC 195
    |||||||
Db 362 ATGTTTCAGGACATC 376

RESULT 15
US-08-468-570-38
; Sequence 38, Application US/08468570
```

```

1 Patent No. 5871962
2
3 GENERAL INFORMATION:
4
5 APPLICANT: BUKH, J., MILLER, R. H. AND
6 APPLICANT: PURCELL, R. H.
7
8 TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
9 TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
10 TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
11 TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
12 TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
13 NUMBER OF SEQUENCES: 159
14
15 CORRESPONDENCE ADDRESS:
16
17 ADDRESSEE: MORGAN & FINNEGAN
18 STREET: 345 PARK AVENUE
19 CITY: NEW YORK
20 STATE: NEW YORK
21 COUNTRY: USA
22
23 ZIP: 10154
24
25 COMPUTER READABLE FORM:
26
27 MEDIUM TYPE: FLOPPY DISK
28 COMPUTER: IBM PC COMPATIBLE
29 OPERATING SYSTEM: PC-DOS/MS-DOS
30 SOFTWARE: WORDPERFECT 5.1
31
32 CURRENT APPLICATION DATA:
33
34 APPLICATION NUMBER: US/08/468,570
35 FILING DATE: 6-JUN-1995
36 CLASSIFICATION: 424
37
38 PRIOR APPLICATION DATA:
39
40 APPLICATION NUMBER: 08/086,428
41 FILING DATE: 29-JUN-1993
42
43 CLASSIFICATION: 424
44
45 ATTORNEY/AGENT INFORMATION:
46
47 NAME: RICHARD W. BORK
48
49 REGISTRATION NUMBER: 36,459
50 REFERENCE/DOCKET NUMBER: 2026-40700S1
51
52 TELECOMMUNICATION INFORMATION:
53
54 TELEPHONE: (212) 758-4800
55 TELEFAX: (212) 751-6849
56
57 TELEX: 421792
58
59 INFORMATION FOR SEQ ID NO: 38:
60
61 SEQUENCE CHARACTERISTICS:
62
63 LENGTH: 576 base pairs
64 TYPE: nucleic acid
65 STRANDEDNESS: single
66
67 TOPOLOGY: linear
68
69 ORIGINAL SOURCE:
70
71 ORGANISM: homosapiens
72
73 INDIVIDUAL ISOLATE: S52
74
75 US-08-468-570-38

```

```
Query Match      3.4%; Score 15; DB 2; Length 576;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 181 ATGTTTCAGGACATC 195  
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 Db 362 ATGTTTCAGGACATC 376

Search completed: November 30, 2002, 02:40:59  
Job time : 67 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 01:37:17 : Search time 2081 seconds  
(without alignments)  
3424.322 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 440  
Sequence: 1 cgtccgcgcgcgcgacttc.....ggaatnntagataaaaaant 440

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST :

1: em\_estba:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 34    | 7.7         | 492    | 10 AW424591 | AW424591 707018G10 |
| 2          | 34    | 7.7         | 646    | 14 BQ487045 | BQ487045 1091050G1 |
| 3          | 34    | 7.7         | 974    | 11 AY108359 | AY108359 Zea mays  |
| 4          | 26    | 5.9         | 491    | 9 AI948185  | AI948185 603037E02 |
| 5          | 26    | 5.9         | 511    | 13 BI233723 | BI233723 949032B03 |
| 6          | 24    | 5.5         | 531    | 10 AW925193 | AW925193 WSI_76_E1 |

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|----|----|-----|-----|----|----------|---------------------|
| 7  | 20 | 4.5 | 243 | 10 | BE511251 | BE511251 946059A03  |
| 8  | 20 | 4.5 | 408 | 9  | A1756562 | A1756562 EteStea02  |
| 9  | 20 | 4.5 | 426 | 10 | BE028394 | BE028394 EteStea77  |
| 10 | 20 | 4.5 | 428 | 13 | BM305795 | BM305795 EteStea40  |
| 11 | 20 | 4.5 | 453 | 17 | BH217843 | BH217843 1006060C1  |
| 12 | 20 | 4.5 | 508 | 10 | BE552951 | BE552951 946087G06  |
| 13 | 20 | 4.5 | 582 | 13 | BM306218 | BM306218 EteStea26  |
| 14 | 20 | 4.5 | 583 | 10 | BE553166 | BE553166 946089H09  |
| 15 | 20 | 4.5 | 585 | 13 | BM306028 | BM306028 EteStea23  |
| 16 | 20 | 4.5 | 604 | 13 | BM305798 | BM305798 EteStea40  |
| 17 | 20 | 4.5 | 616 | 9  | A1757288 | A1757288 EteStea14  |
| 18 | 20 | 4.5 | 991 | 11 | AY104688 | AY104688 Zea mays   |
| 19 | 19 | 4.3 | 150 | 13 | BI233722 | BI233722 949032B03  |
| 20 | 19 | 4.3 | 287 | 9  | AU088613 | AU088613 AU088613   |
| 21 | 19 | 4.3 | 288 | 10 | AW758690 | AW758690 NXNV_085   |
| 22 | 19 | 4.3 | 359 | 9  | AU065686 | AU065686 AU065686   |
| 23 | 19 | 4.3 | 360 | 10 | BE638916 | BE638916 946015F12  |
| 24 | 19 | 4.3 | 412 | 12 | BG039388 | BG039388 NXSI_098   |
| 25 | 19 | 4.3 | 437 | 9  | A1941641 | A1941641 618032F03  |
| 26 | 19 | 4.3 | 501 | 12 | BF221174 | BF221174 NXCI_164   |
| 27 | 19 | 4.3 | 528 | 13 | BM187966 | BM187966 saJ8b10    |
| 28 | 19 | 4.3 | 545 | 14 | BQ699897 | BQ699897 NXRVI31    |
| 29 | 19 | 4.3 | 558 | 14 | BQ290844 | BQ290844 NXRVI050   |
| 30 | 19 | 4.3 | 600 | 10 | BE511573 | BE511573 946061H05  |
| 31 | 19 | 4.3 | 617 | 13 | BM427811 | BM427811 NXRVI_003  |
| 32 | 19 | 4.3 | 649 | 13 | BM332865 | BM332865 MEST180-E  |
| 33 | 19 | 4.3 | 686 | 14 | BQ654835 | BQ654835 NXRVI086-C |
| 34 | 19 | 4.3 | 713 | 14 | BQ291333 | BQ291333 NXRVI058-H |
| 35 | 19 | 4.3 | 779 | 14 | BQ700058 | BQ700058 NXRVI134-C |
| 36 | 19 | 4.3 | 788 | 14 | BQ698967 | BQ698967 NXRVI17-F  |
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| 38 | 18 | 4.1 | 325 | 13 | BM153443 | BM153443 TCBAF2D12  |
| 39 | 18 | 4.1 | 351 | 17 | AQ843815 | AQ843815 LMAJFV1_1  |
| 40 | 18 | 4.1 | 360 | 9  | AJ465631 | AJ465631 AJ465631   |
| 41 | 18 | 4.1 | 375 | 17 | BH221877 | BH221877 1006103H0  |
| 42 | 18 | 4.1 | 375 | 17 | BH222004 | BH222004 1006104F0  |
| 43 | 18 | 4.1 | 383 | 10 | BE238451 | BE238451 946001B08  |
| 44 | 18 | 4.1 | 401 | 10 | BE125828 | BE125828 DGI_58-B0  |
| 45 | 18 | 4.1 | 429 | 17 | PL15L    | ALI60507 Leishmani  |

#### ALIGNMENTS

RESULT 1  
AW424591  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AW424591 707018G1.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea  
mays cDNA, mRNA sequence.  
AW424591 707018G1.1 GI:6952523  
EST.  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade: Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 492)  
Walbot,V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 707018 row: G column: 10.  
Location/Qualifiers  
1. .492  
/organism="Zea mays"

```

/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707" - Mixed adult tissues from Walbot lab (SK
)
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
BASE COUNT      89 a  146 c  149 g  106 t
ORIGIN
Query Match      7.7%; Score 34; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 53
|||||
DB 40 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 73
|||||

RESULT 2
BQ487045      646 bp  mRNA  linear  EST 07-JUN-2002
LOCUS
DEFINITION
Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION
BQ487045
VERSION
BQ487045.1 GI:21331664
KEYWORDS
EST.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 646)
AUTHORS
Walbot,V.
TITLE
Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091050 row: G column: 11.
Location/Qualifiers
1. .646
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="1091" - Immature ear with common ESTs screened
by Schmidt lab"
/tissue_type="Inflorescence meristem - floral organ
primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
/notes="Organ: Immature ear; Vector: PAD-GAL4; Site_1:
EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
BASE COUNT      130 a  165 c  198 g  153 t
ORIGIN
Query Match      7.7%; Score 34; DB 14; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
DB 40 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 73
|||||

/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707" - Mixed adult tissues from Walbot lab (SK
)
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
BASE COUNT      89 a  146 c  149 g  106 t
ORIGIN
Query Match      7.7%; Score 34; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 53
|||||
DB 40 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 73
|||||

RESULT 3
AY108359      974 bp  mRNA  linear  HTC 25-MAY-2002
LOCUS
DEFINITION
Zea mays PC0061446 mRNA sequence.
ACCESSION
AY108359
VERSION
AY108359.1 GI:21211437
KEYWORDS
HTC.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 974)
AUTHORS
Halney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whittsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL
Unpublished (2002)
REFERENCE
2 (bases 1 to 974)
AUTHORS
Coe,E.C.
TITLE
Direct Submission
JOURNAL
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. .974
/organism="Zea mays"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT      235 a  234 c  257 g  248 t
ORIGIN
Query Match      7.7%; Score 34; DB 11; Length 974;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 53
|||||
DB 45 CGCCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCC 78
|||||

RESULT 4
AI948185      491 bp  mRNA  linear  EST 19-AUG-1999
LOCUS
DEFINITION
603037E02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
Zea mays cDNA, mRNA sequence.
ACCESSION
AI948185
VERSION
AI948185.1 GI:5740495
KEYWORDS
EST.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 491)
AUTHORS
Walbot,V.
TITLE
Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
Unpublished (1999)
JOURNAL
Contact: Walbot V
Department of Biological Sciences
Stanford University
```



855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 603037 row: E column: 02.

#### FEATURES

source

Location/Qualifiers

1. 491  
 /organism="Zea mays"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="603 - stressed root cDNA library from Wang/Bohnert lab"  
 /tissue\_type="seedling"  
 /dev\_stage="salt stress"  
 /lab\_host="E. coli XL Gold"  
 /note="Organ: root; Vector: pBluescriptII SK(+/-) XR; Seedling stressed root cDNA library from Wang/Bohnert lab"  
 76 a 165 c 148 g 100 t  
 2 others

BASE COUNT 76 a 165 c 148 g 100 t

ORIGIN

Query Match 5.9%; Score 26; DB 9; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 0.00071;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AGGCAGCGGTGGTGGCGATGGCGT 109  
 |||||  
 Db 246 AGGCAGCGGTGGTGGCGATGGCGT 271

#### RESULT 5

LOCUS

DEFINITION B1233723 511 bp mRNA linear EST 11-JUL-2001  
 Zea mays cDNA, mRNA sequence.

ACCESSION B1233723

VERSION B1233723.1

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

AUTHORS clade: Panicoideae; Andropogoneae; Zea.

TITLE 1 (bases 1 to 511)

COMMENT Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 949032 row: B column: 03.

Location/Qualifiers

1. 511

/organism="Zea mays"

/cultivar="W64A"

/db\_xref="taxon:4577"

/clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve

Moose"

/tissue\_type="Immature leaf primordium and vegetative

meristem"

/dev\_stage="4 stages from 3-13 days after imbibing"

/lab\_host="E. coli XL0LR"

/note="Organ: Juvenile vegetative shoots; Vector:

PAD-GAU4-2.1; Site: EcoRI; Site: XhoI; Equal amounts

of total RNA by weight from 4 tissue sources (see below)

were pooled, polyA+ RNA isolated, and cDNA synthesized for

EcoRI (5') and XhoI (3') directional cloning into lambda

Hybridap vector from Stratagene. Tissue Sources: 1. Whole

shoots 3 days after sowing/imbibing in wet soil. 2. Basal

1.5 cm shoots 6 days after sowing - includes yellow  
 portions of developing leaves 1-5, primordia from 6-8, and  
 the vegetative apex. 3. Non-green portions of developing  
 leaves 4-5 and the vegetative apex, including adult leaf  
 primordia, 9 days after sowing. 4. Partially expanded and  
 greening leaves 4-5 at 13 days after sowing."

BASE COUNT 105 a 130 c 156 g 120 t

ORIGIN

Query Match 5.9%; Score 26; DB 13; Length 511;

Best Local Similarity 100.0%; Pred. No. 0.00071;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AGGCAGCGGTGGTGGCGATGGCGT 109

|||||

Db 47 AGGCAGCGGTGGTGGCGATGGCGT 72

|||||

RESULT 6

LOCUS AW925193

DEFINITION WS1\_76\_E10.b1\_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,

mRNA sequence.

ACCESSION AW925193

VERSION AW925193.1

KEYWORDS EST.

SOURCE Sorghum.

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

REFERENCE 1 (bases 1 to 531)

AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt

L.H.

An EST database from Sorghum: water-stressed plants

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: JEN REV

High quality sequence stop: 458

POLYA-No.

Location/Qualifiers

1. 531

/organism="Sorghum bicolor"

/db\_xref="taxon:4558"

/clone\_lib="Water-stressed 1 (WS1)"

/note="Organ: Mix of 5-week old plants on days 7 & 8 after

water was withheld; Vector: Lambda Zap; Site: 1. XhoI;

Site: 2. EcoRI; The library was made from polyA RNA in the

cloning vector lambda Zap II. Clones to be sequenced were

prepared by mass excision."

BASE COUNT 107 a 156 c 164 g 104 t

ORIGIN

Query Match 5.5%; Score 24; DB 10; Length 531;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGCAGCGGTGGTGGCGATGGCGT 109

|||||

Db 175 GGCAGCGGTGGTGGCGATGGCGT 198

|||||

RESULT 7

BES11251

LOCUS BE511251 243 bp mRNA linear EST 07-AUG-2000  
 DEFINITION 946059A03.y1.946 - tassal primordium prepared by Schmidt lab Zea  
 mays cDNA, mRNA sequence.  
 ACCESSION BE511251  
 VERSION BE511251.1 GI:9732499  
 KEYWORDS EST.  
 ORGANISM Zea mays.  
 Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 243)  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 JOURNAL University  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946059 row: A column: 03.  
 FEATURES  
 source Location/Qualifiers  
 1..243  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="946 - tassal primordium prepared by Schmidt  
 lab"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="XLOLR"  
 /note="Organ: tassels; Vector: HybriZAP; Site\_1: EcoRI;  
 Site\_2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybriZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."  
 BASE COUNT 29 a 93 c 74 g 47 t  
 ORIGIN  
 Query Match 4.5%; Score 20; DB 10; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 20 CGCCTTTTCGTCGCCGCGTC 39  
 |||||||||||||||||||||  
 Db 16 CGCCTTTTCGTCGCCGCGTC 35  
 |||||||||||||||||||||  
 RESULT 8  
 A1756562 408 bp mRNA linear EST 18-JAN-2000  
 LOCUS EteStea02a09.y1 Elmeria M5-6 Merozoite stage Elmeria tenella cDNA  
 DEFINITION 5' similar to SW:R141\_MAIZE P19950 40S RIBOSOMAL PROTEIN S14 ;,  
 mRNA sequence.  
 ACCESSION A1756562  
 VERSION A1756562.1 GI:5150285  
 KEYWORDS EST.  
 SOURCE Elmeria tenella.  
 ORGANISM Elmeria tenella.  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;  
 Elmeria.  
 REFERENCE 1 (bases 1 to 408)  
 AUTHORS Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,  
 Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen  
 ,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey  
 ,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson  
 ,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.  
 WashU-Merck Elmeria tenella project  
 Unpublished (1999)  
 TITLE WashU-Merck Elmeria tenella project  
 JOURNAL

COMMENT Contact: David Sibley, Ph.D.  
 WashU-Merck Elmeria tenella project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Contact David Sibley (toxoe@borcim.wustl.edu) for further  
 information relating to organism, libraries, or clone availability.  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 393.  
 FEATURES  
 source Location/Qualifiers  
 1..408  
 /organism="Elmeria tenella"  
 /strain="LS18"  
 /db\_xref="taxon:5802"  
 /clone\_lib="Elmeria M5-6 Merozoite stage"  
 /dev\_stage="Merozoite"  
 /lab\_host="SOLR E. coll"  
 /note="Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI  
 ; Merozoites were obtained from ceacal scrapings of  
 chickens infected with E. tenella. The library may  
 contain a small percentage of host or bacterial  
 contaminants. cDNA was synthesized from poly mRNA using  
 an oligo-dT primer containing a XhoI site. Following to  
 second strand synthesis, EcoRI adapters were ligated to  
 the cDNA and products were size-selected on Sephacryl  
 S500. cDNAs were digested with EcoRI/XhoI and cloned into  
 lambda zap II (Stratagene). Clones were converted to  
 phagemids by mass excision using ExAssist helper phage and  
 SOLR cells (Stratagene). Insert sizes range from 0.7-1.5  
 kb."  
 BASE COUNT 73 a 156 c 129 g 50 t  
 ORIGIN  
 Query Match 4.5%; Score 20; DB 9; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 60 CGTGGCGTCACCGCGGCA 79  
 |||||||||||||||||||||  
 Db 138 CGTGGCGTCACCGCGGCA 157  
 |||||||||||||||||||||  
 RESULT 9  
 BE028394 426 bp mRNA linear EST 07-JUN-2000  
 LOCUS EteStea77f06.y1 Elmeria M5-6 Merozoite stage substracted Elmeria  
 tenella cDNA 5' similar to SW:R141\_MAIZE P19950 40S RIBOSOMAL  
 PROTEIN S14 ;, mRNA sequence.  
 ACCESSION BE028394  
 VERSION BE028394.1 GI:8321824  
 KEYWORDS EST.  
 SOURCE Elmeria tenella.  
 ORGANISM Elmeria tenella.  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;  
 Elmeria.  
 REFERENCE 1 (bases 1 to 426)  
 AUTHORS Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,  
 Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen  
 ,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey  
 ,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson  
 ,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.  
 WashU-Merck Elmeria tenella project  
 Unpublished (1999)  
 TITLE WashU-Merck Elmeria tenella project  
 JOURNAL  
 COMMENT Contact: David Sibley, Ph.D.  
 WashU-Merck Elmeria tenella project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Contact David Sibley (toxost@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 423.

## FEATURES

source

```
1. 426
/organism="Eimeria tenella"
/db_xref="taxon:5802"
/clone_lib="Eimeria M5-6 Merozoite stage subtracted"
/dev_stage="Merozoite"
/lab_host="SOLR E. coli"
/notes="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Merozoites were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-dT primer containing a XhoI
site. Following second strand synthesis, EcoRI adapters
were ligated to the cDNA and products were size-selected
on Sephadryl S500. The cDNAs were ligated to EcoRI/XhoI
prepared lambda ZAPII(Stratagene). Clones were converted
to phagemids by mass excision using ExAssist helper phage
and E.coli SOLR cells (Stratagene). Insert sizes range
from 0.7-1.5Kb. The library may contain a small percentage
of host or bacterial contaminants. Clones were selected by
negative hybridization against a pool of over-represented
ESTs (N>=10, from 1506 previous reads)."
76 a 153 c 141 g 56 t
```

## BASE COUNT

ORIGIN

```
Query Match 4.5%; Score 20; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 60 CGTGGCGTCACCGCGGCA 79

|||||

Db 67 CGTGGCGTCACCGCGGCA 86

## RESULT 10

BM305795

LOCUS

DEFINITION

BM305795 428 bp mRNA linear EST 02-JAN-2002  
ETESTee40f01.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria  
tenella cDNA 5' similar to SW:RS14\_CAERL P48150 PROBABLE 40S  
RIBOSOMAL PROTEIN S14. [1] ; mRNA sequence.

ACCESSION

BM305795

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;

Eimeria.

REFERENCE

AUTHORS

1 (bases 1 to 428)

TITLE

JOURNAL

COMMENT

WashU-Merck Eimeria tenella project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Contact David Sibley (toxost@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 367.  
Location/Qualifiers  
1. 428  
/organism="Eimeria tenella"

## FEATURES

source

```
/strain="LS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria tenella M5-6 cDNA Neg Selected"
/dev_stage="Merozoite"
/lab_host="DH10B (GENEHOG, E.coli HS996)"
/notes="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Merozoites were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-dT primer containing a XhoI
site. Following second strand synthesis, EcoRI adapters
were ligated to the cDNA and products were size-selected
on Sephadryl S500. The cDNAs were ligated to EcoRI/XhoI
prepared lambda ZAPII(Stratagene). Clones were converted
to phagemids by mass excision using ExAssist helper phage
and E.coli SOLR cells (Stratagene). Clones were selected
by negative hybridization against a pool of
over-represented ESTs (N>=10, from 1506 previous reads),
and transformed to DH10B (GENEHOGS, STRATAGENE). The
library may contain a small percentage of host or
bacterial contaminants."
66 a 128 c 154 g 80 t
```

## BASE COUNT

ORIGIN

```
Query Match 4.5%; Score 20; DB 13; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 60 CGTGGCGTCACCGCGGCA 79

|||||

Db 347 CGTGGCGTCACCGCGGCA 366

## RESULT 11

BH217843

LOCUS

DEFINITION

BH217843 453 bp DNA linear GSS 08-NOV-2001  
1006060C11.y1 1006 - RescueMu Grid G Zea mays genomic, DNA  
sequence.

ACCESSION

BH217843

VERSION

BH217843.1

KEYWORDS

GSS.

SOURCE

Zea mays.

ORGANISM

Zea mays.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Plate: 1006060 row: 8  
Class: transposon-tagged.  
Location/Qualifiers  
1. 453  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - RescueMu Grid G"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"

## FEATURES

source

pBlueScript backbone); Site\_1: BamHI; Site\_2: BglII;  
RescueMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

58 a 150 c 133 g 112 t

Query Match 4.5%; Score 20; DB 17; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AGCGGAGGCGCGGTGGT 98  
|||||  
Db 109 AGCGGAGGCGCGGTGGT 128  
|||||

RESULT 12  
BE552951  
LOCUS  
DEFINITION 508 bp mRNA linear EST 10-AUG-2000  
mays cDNA, mRNA sequence.  
ACCESSION BE552951  
VERSION BE552951.1 GI:9794643  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays

REFERENCE  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 946087 row: G column: 06.  
Location/Qualifiers  
1. 508  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassels primordium prepared by Schmidt lab"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to inflorescence development"  
/lab\_host="XLOLR"  
/note="Organ: tassels; Vector: HybriZAP; Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."  
BASE COUNT 98 a 143 c 149 g 118 t

Query Match 4.5%; Score 20; DB 10; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AGCGGAGGCGCGGTGGT 98  
|||||  
Db 59 AGCGGAGGCGCGGTGGT 78  
|||||

RESULT 13  
BM306218  
LOCUS  
DEFINITION 582 bp mRNA linear EST 02-JAN-2002  
EteEstee2607.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria tenella cDNA 5' similar to SW:R141\_MAIZE P19950 40S RIBOSOMAL PROTEIN S14 ;, mRNA sequence.  
ACCESSION BM306218  
VERSION BM306218.1 GI:18037924  
KEYWORDS EST.  
SOURCE Eimeria tenella.  
ORGANISM Eimeria tenella  
REFERENCE  
AUTHORS 1 (bases 1 to 582)  
Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D. WashU-Merck Eimeria tenella project  
Unpublished (1999)  
Contact: David Sibley, Ph.D.  
WashU-Merck Eimeria tenella project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Contact David Sibley (toxoe@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 412.  
Location/Qualifiers  
1. 582  
/organism="Eimeria tenella"  
/strain="LS18"  
/db\_xref="taxon:5802"  
/clone\_lib="Eimeria tenella M5-6 cDNA Neg Selected"  
/dev\_stage="Merzoite"  
/lab\_host="DH10B (GENEHOG, E.coli HS996)"  
/note="Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI ; Merzoites were obtained from ceasal scrapings of chickens infected with E. tenella. cDNA was synthesized from poly mRNA using an oligo-dr primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephacryl S500. The cDNAs were ligated to EcoRI/XhoI prepared lambda ZAPII(Stratagene). Clones were converted to phagemids by mass excision using ExAssist helper phage and E.coli SOLR cells (Stratagene). Clones were selected by negative hybridization against a pool of over-represented ESTs (N>=10, from 1506 previous reads), and transformed to DH10B (GENEHOGS, STRATAGENE). The library may contain a small percentage of host or bacterial contaminants."

BASE COUNT 89 a 189 c 212 g 91 t 1 others

Query Match 4.5%; Score 20; DB 13; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CGTGGCGGTACCGCGGCA 79  
|||||  
Db 339 CGTGGCGGTACCGCGGCA 358  
|||||

RESULT 14  
BE553166  
LOCUS  
DEFINITION 583 bp mRNA linear EST 10-AUG-2000  
946089H09.y1 946 - tassels primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

```

ACCESSION BE553166
VERSION BE553166.1 GI:9794858
KEYWORDS EST
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 583)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946089, row: H column: 09.
FEATURES
Location/Qualifiers
1..583
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassels primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOR"
/Note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."
BASE COUNT 114 a 157 c 175 g 137 t
ORIGIN
Query Match 4.58; Score 20; DB 10; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 CGCCTTTTCGTCGCCGCGTC 39
|||||
Db 6 CGCCTTTTCGTCGCCGCGTC 25

RESULT 15
BM306028
LOCUS BM306028
DEFINITION EStEE23g03.y1 Eimeria tenella M5-6 cDNA Neg Selected Eimeria
tenella cDNA 5' similar to SW:R141_MAIZE P19950 40S RIBOSOMAL
PROTEIN S14 ; mRNA sequence.
ACCESSION BM306028
VERSION BM306028.1 GI:18037734
KEYWORDS EST
SOURCE Eimeria tenella.
ORGANISM Eimeria tenella.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
REFERENCE 1 (bases 1 to 585)
AUTHORS Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen
M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey
N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,R., Jackson
Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D.
WashU-Merck Eimeria tenella project
Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Contact David Sibley (toxest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 378.
Location/Qualifiers
1..585
/organism="Eimeria tenella"
/strain="LS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria tenella M5-6 cDNA Neg Selected"
/dev_stage="Merzoite"
/lab_host="DH10B (GENEHOG, E.coli HS996)"
/Note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI
; Merzoites were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-dT primer containing a XhoI
site. Following second strand synthesis, EcoRI adapters
were ligated to the cDNA and products were size-selected
on Sephacryl S500. The cDNAs were ligated to EcoRI/XhoI
prepared lambda ZAPII(Stratagene). Clones were converted
to phagemids by mass excision using EXAssist helper phage
and E.coli SOLR cells (Stratagene). Clones were selected
by negative hybridization against a pool of
over-represented ESTs (N=10, from 1506 previous reads),
and transformed to DH10B (GENEHOGS, STRATAGENE). The
library may contain a small percentage of host or
bacterial contaminants."
BASE COUNT 90 a 188 c 208 g 95 t 4 others
ORIGIN
Query Match 4.58; Score 20; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 CGTGGCGGTGTCACCGCGGCA 79
|||||
Db 354 CGTGGCGGTGTCACCGCGGCA 373

Search completed: November 30, 2002, 04:01:12
Job time : 2095 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 02:35:57 ; Search time 56 Seconds

(without alignments)

3025.907 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtcgcgcgcgcgcacttc.....ggaatnntagataaaaaant 440

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 341543 seqs, 192557720 residues

Word size : 0

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 26    | 5.9         | 216    | 10 | US-09-923-876-28    |
| 2          | 18    | 4.1         | 255    | 10 | US-09-923-876-6319  |
| 3          | 17    | 3.9         | 761    | 12 | US-10-062-254-55    |
| 4          | 17    | 3.9         | 1612   | 12 | US-10-062-254-57    |
| 5          | 16    | 3.6         | 250    | 10 | US-09-878-574-10592 |
| 6          | 16    | 3.6         | 286    | 9  | US-09-924-400-17    |
| 7          | 16    | 3.6         | 286    | 10 | US-09-810-936-17    |
| 8          | 16    | 3.6         | 286    | 10 | US-09-429-755-17    |
| 9          | 16    | 3.6         | 900    | 10 | US-09-815-242-6108  |
| c 10       | 16    | 3.6         | 939    | 9  | US-09-938-842A-2421 |
| c 11       | 16    | 3.6         | 1866   | 10 | US-09-802-674-1     |
| c 12       | 16    | 3.6         | 1870   | 9  | US-09-981-353-109   |
| c 13       | 16    | 3.6         | 1998   | 10 | US-09-815-242-7695  |
| c 14       | 16    | 3.6         | 2000   | 9  | US-09-938-842A-4602 |
| 15         | 16    | 3.6         | 2208   | 10 | US-09-815-242-7991  |
| 16         | 16    | 3.6         | 3119   | 10 | US-09-867-701-10873 |
| 17         | 16    | 3.6         | 3123   | 10 | US-09-912-020-122   |
| 18         | 16    | 3.6         | 3123   | 10 | US-09-815-242-6106  |
| 19         | 16    | 3.6         | 13029  | 10 | US-09-815-242-4052  |

|      |    |     |       |    |                     |
|------|----|-----|-------|----|---------------------|
| c 20 | 16 | 3.6 | 20633 | 10 | US-09-070-927A-276  |
| c 21 | 15 | 3.4 | 36    | 10 | US-09-973-322-15    |
| c 22 | 15 | 3.4 | 203   | 10 | US-09-294-093B-4713 |
| c 23 | 15 | 3.4 | 276   | 10 | US-09-294-093B-5682 |
| c 24 | 15 | 3.4 | 281   | 10 | US-09-294-093B-5703 |
| c 25 | 15 | 3.4 | 283   | 10 | US-09-294-093B-4681 |
| c 26 | 15 | 3.4 | 288   | 10 | US-09-294-093B-1526 |
| c 27 | 15 | 3.4 | 296   | 10 | US-09-294-093B-6090 |
| c 28 | 15 | 3.4 | 300   | 10 | US-09-974-300-8146  |
| c 29 | 15 | 3.4 | 301   | 10 | US-09-864-761-24056 |
| c 30 | 15 | 3.4 | 402   | 10 | US-09-974-300-1897  |
| c 31 | 15 | 3.4 | 439   | 10 | US-09-604-287A-149  |
| c 32 | 15 | 3.4 | 439   | 10 | US-09-339-338-149   |
| c 33 | 15 | 3.4 | 439   | 12 | US-10-007-805-149   |
| c 34 | 15 | 3.4 | 472   | 10 | US-09-974-300-6336  |
| c 35 | 15 | 3.4 | 556   | 10 | US-09-864-761-7326  |
| c 36 | 15 | 3.4 | 597   | 9  | US-09-727-855B-6    |
| c 37 | 15 | 3.4 | 817   | 10 | US-09-925-301-165   |
| c 38 | 15 | 3.4 | 1035  | 9  | US-09-712-363-83    |
| c 39 | 15 | 3.4 | 1109  | 9  | US-09-938-842A-3333 |
| c 40 | 15 | 3.4 | 1119  | 10 | US-09-921-992-3     |
| c 41 | 15 | 3.4 | 1191  | 10 | US-09-741-669-223   |
| c 42 | 15 | 3.4 | 1311  | 10 | US-09-790-264-31    |
| c 43 | 15 | 3.4 | 1440  | 10 | US-09-790-264-40    |
| c 44 | 15 | 3.4 | 1686  | 10 | US-09-812-079A-1    |
| c 45 | 15 | 3.4 | 1773  | 10 | US-09-815-242-4044  |

#### ALIGNMENTS

##### RESULT 1

US-09-923-876-28

; Sequence 28, Application US/09923876

; Patent No. US20020013958A1

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Kamigaki, Laura Y. (Ito)

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

; FILE REFERENCE: PL-0012-1 COM

; CURRENT APPLICATION NUMBER: US/09/923,876

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: 09/298,329

; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: 60/085,331

; PRIOR FILING DATE: 1998-05-05

; NUMBER OF SEQ ID NOS: 6332

; SOFTWARE: PERL Program

; SEQ ID NO 28

; LENGTH: 216

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. US20020013958A1 700142447H1

US-09-923-876-28

Query Match 5.9% Score 26; DB 10; Length 216;

Best Local Similarity 100.0%; Pred. No. 5.2e+06;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 84 AGGCAGCGCGTGTGGCGATGGCGT 109

|||||

Db 3 AGGCAGCGCGTGTGGCGATGGCGT 28

##### RESULT 2

US-09-923-876-6319

; Sequence 6319, Application US/09923876

; Patent No. US20020013958A1

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.

```
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6319
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458871H1
US-09-923-876-6319

Query Match          4.1%; Score 18; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 86 GGCAGCGGTGGTGGCGA 103
      |||||
DB 169 GGCAGCGGTGGTGGCGA 186

RESULT 3
US-10-062-254-55
; Sequence 55, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Oryza sativa
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; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (69)
; NAME/KEY: unsure
; LOCATION: (73)
US-10-062-254-55

Query Match          3.9%; Score 17; DB 12; Length 761;
Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 66 CGTCACGGCGCGCAGGC 82
      |||||
DB 84 CGTCACGGCGCGCAGGC 100

RESULT 4
US-10-062-254-57
; Sequence 57, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Oryza sativa
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US-10-062-254-57

Query Match 3.6%; Score 17; DB 12; Length 1612;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 CGTCACGGCGGCAGGC 82  
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DB 91 CGTCACGGCGGCAGGC 107

## RESULT 5

US-09-878-574-10592  
; Sequence 10592, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 10592  
; LENGTH: 250  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700966847H1  
US-09-878-574-10592

Query Match 3.6%; Score 16; DB 10; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 GCGGGTGGTGGCGATG 105  
|||||  
DB 162 GCGGGTGGTGGCGATG 177

## RESULT 6

US-09-924-400-17  
; Sequence 17, Application US/09924400  
; Patent No. US20020165371A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Smith, John M.  
; APPLICANT: Mishner, Lynda E.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.419C12  
; CURRENT APPLICATION NUMBER: US/09/924,400  
; CURRENT FILING DATE: 2001-08-07  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-924-400-17

Query Match 3.6%; Score 16; DB 9; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGGCG 108  
|||||  
DB 172 GGTGGTGGCGATGGCG 187

## RESULT 7

US-09-810-936-17  
; Sequence 17, Application US/09810936  
; Patent No. US20020068285A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Smith, John M.  
; APPLICANT: Mishner, Lynda E.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Day, Craig H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.419C11  
; CURRENT APPLICATION NUMBER: US/09/810,936  
; CURRENT FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-810-936-17

Query Match 3.6%; Score 16; DB 10; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGTGGTGGCGATGGCG 108  
|||||  
DB 172 GGTGGTGGCGATGGCG 187

## RESULT 8

US-09-429-755-17  
; Sequence 17, Application US/09429755A  
; Patent No. US2002011467A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Mishner, Lynda  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.419C6  
; CURRENT APPLICATION NUMBER: US/09/429,755A  
; CURRENT FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-429-755-17

Query Match 3.6%; Score 16; DB 10; Length 286;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US200201

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; PRIOR APPLICATION NUMBER: US 60/227,869

[illegible]





## SUMMARIES

pred. No. is the number of results predicted by chance to have a

AB012046 975 bp mRNA linear PLN 05-AUG-2000  
Hordeum vulgare HvAPRT1 mRNA for Adenine phosphoribosyltransferase,  
complete cds.  
AB012046  
AB012046.1 GI:9711920  
HvAPRT1; Adenine phosphoribosyltransferase.  
Hordeum vulgare (variety:Elmhada no.1) root cDNA to mRNA.  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticeae; Hordeum.  
1 (sites)  
Ital.,R., Suzuki,K., Yamauchi,H., Nakanishi,H., Nishizawa,N.K.,

## ALIGNMENTS

QY 90 GCGGTGGTGGCGATG 105  
| | | | | | | | | | | | | |  
Db 1149 GCGGTGGTGGCGATG 1164

Search completed: November 30, 2002, 04:02:23  
Job time : 63 secs

US-09-981-353-109

Query Match 3.6%; Score 16; DB 9; Length 1870;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GCGAGCGGTGGTGGC 101  
|||||

Db 736 GCGAGCGGTGGTGGC 721

RESULT 13

US-09-815-242-7695  
Sequence 7695, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

SOFTWARE: FastSEQ for Windows Version 4.0

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO 7695

LENGTH: 1998

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1998)

US-09-815-242-7695

Query Match 3.6%; Score 16; DB 10; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCGGCGCGACTTGGCC 23  
|||||

Db 996 GCGGCGCGACTTGGCC 1011

RESULT 14

US-09-938-842A-4602/c

Sequence 4602, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPI300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 4602

LENGTH: 2000

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-4602

Query Match 3.6%; Score 16; DB 9; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 ACCATTTTGTCAAGCG 254  
|||||

Db 1871 ACCATTTTGTCAAGCG 1856

RESULT 15

US-09-815-242-7991

Sequence 7991, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7991

LENGTH: 2208

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(2208)

US-09-815-242-7991

Query Match 3.6%; Score 16; DB 10; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 310 CCA-TGAGGAGCCCAAGAGCTACTCGGAAGGTTATTTTCGGAGGAGTATTCGTTGGA 368

Qy 415 GAATNNGGAATNTAGATAAAAA 437

Db 369 GTATGGAACAGATACGATTGAGA 391

RESULT 6

AY128377 887 bp mRNA linear PLN 07-AUG-2002

LOCUS Arabidopsis thaliana adenine phosphoribosyltransferase 1, APRT

DEFINITION Arabidopsis thaliana complete cds.

ACCESSION AY128377

VERSION AY128377.1 GI:22135995

KEYWORDS FLI\_CDNA.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 887)

REFERENCE Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA': Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, P0EC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Tripp,M., Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Tripp,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source 1..887

location/Qualifiers

1..887

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/chromosome="1"

/clone="RAFL11-04-P04 (R15127)"

/note="This clone is in pBluescript

ecotype: Columbia"

1..887

/gene="Atlg27450"

46..597

/gene="Atlg27450"

/codon\_start=1

/product="adenine phosphoribosyltransferase 1, APRT"

/protein\_id="AA091580.1"

/db\_xref="GI:22135996"

/translation="MATEDVQDPRIAKIASSIRVDPFKPGIMFQDITLLILDEAF KDIAFLVDYKDKGISVAVGARGIFGPPIALAIKAIFVPMRKPPLKPKVISEE YSLFYGDTTETHVGVAVEGERAIIDDLIATGGTLLAAAILRLRVGVKIVECACVIE LPELKGKEKIGETSLFVLYKSA"

BASE COUNT 234 a 157 c 224 g 272 t

ORIGIN

Query Match 19.7%; Score 86.6; DB 8; Length 887;

Best Local Similarity 55.7%; Pred No. 8.7e-10;

Matches 180; Conservative 0; Mismatches 139; Indels 4; Gaps 3;

Qy 115 GATCCCGCGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCGACTTNCCAAAGCCA 174

Db 67 GATCCCAAGATCGTATAGATTGCTCTTCCATTAGAGTATCCCGGACTTCCCTAAACCA 126

Qy 175 GGGATNATGTTTCAGGACATCANGNTGTTTCGATCCCAAGGCGTCCGTCGACAAC 234

Db 127 GGAATCATGTTTCAGGACATACAGAGCTTCTTCGACACTGAGGCTTTAAGGATACT 186

Qy 235 ATATACCATTTTCTCAAGCGGTACAAGCAACAGGATCACCTTGGAAATAGAGGTAA 294

Db 187 ATTGCTTTGTTTGTGATAGATACAAAGATAGCATATCTGTG-TTGCAAGGTGTA 245

Qy 295 AGCTAGAGGNTCANTTTTCGGAACACTANNCTTANAANNAATTTGGTCAAAATNGGTG 354

Db 246 AGCTAGAGGTTCTATTTTGGCCCTCTATTCGGTGG--GCTATGTCGCCAAATTTGTT 303

Qy 355 NCNATTGAGGAACNNATNAGNCCANGCCNAAATGATTTTNGAATANGAATTTTGG 414

Db 304 CCA-TGAGGAAGCCCAAGAGTACCTCGGAAGGTTATTTTCGGAGGAGTATTCGTTGGA 362

Qy 415 GAKTNNNGAATNTAGATAAAAA 437

Db 363 GTAAGGACAGATACGATTGAGA 385

RESULT 7

AY084513 847 bp mRNA linear PLN 21-JUN-2002

LOCUS Arabidopsis thaliana clone 11009 mRNA, complete sequence.

DEFINITION Arabidopsis thaliana clone 11009 mRNA, complete sequence.

ACCESSION AY084513

VERSION AY084513.1 GI:21403223

KEYWORDS FLI\_CDNA.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 847)

REFERENCE Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

AUTHORS Full-length messenger RNA sequences greatly improve genome annotation

TITLE Genome Biol. (2002) In press

JOURNAL 2 (bases 1 to 847)

REFERENCE Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

AUTHORS Full-length cDNA from Arabidopsis thaliana

TITLE Unpublished

JOURNAL 3 (bases 1 to 847)

REFERENCE Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

AUTHORS Direct Submission

TITLE Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

JOURNAL This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

| FEATURES              |     | Location/Qualifiers  |     |
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|                       |     | /chromosome="4"  |     |
|                       |     | /clone="C103141 (B)"   |     |
|                       |     | /note="This clone is in puni 51."                                  |     |
|                       |     | ecotype: Columbia  |     |
| gene                  |     | 1..579   |     |
|                       |     | /gene="At4g12440"  |     |
| CDS                   |     | 1..549   |     |
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|                       |     | /codon_start=1   |     |
|                       |     | /evidence=experimental   |     |
|                       |     | /product="putative adenine phosphoribosyltransferase"              |     |
|                       |     | /protein_id="AA091623.1"   |     |
|                       |     | /db_xref="GI:22136608"   |     |
|                       |     | /translation="MSENVDDPRIDGIRKRVVDPFKKGFIMFQDITVLLDPKAF             |     |
|                       |     | KPTIDLFVRYRDMNISVAGIEARGFPGPIALAIKAKEVPLRKPGLPGQIFEE               |     |
|                       |     | YELEYGSDRLMHVAVSDGRALVDDLIATGTCANMNLKRVGAIEVCACVIE                 |     |
|                       |     | LPELKGRELEKRPILVLYEYR"   |     |
| 3'UTR                 |     | 550..579   |     |
|                       |     | /gene="At4g12440"  |     |
|                       |     | /misc_difference 564..565  |     |
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| ORIGIN                |     |  |     |
| Query Match           |     | 16.5%; Score 72.4; DB 8; Length 579;                               |     |
| Best Local Similarity |     | 52.6%; Pred. No. 1.6e-06;  |     |
| Matches               |     | 159; Conservative 0; Mismatches 140; Indels 3; Gaps 2;             |     |
| QY                    | 115 | GATCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTMATNCCGACTTCCAAAGCCA          | 174 |
| DB                    | 22  | GATCTCTGATCGATGTGTATCAAAATAGATCCGTGCTCCAGATTTCCCAAGAAA             | 81  |
| QY                    | 175 | GGATNATGTTTCAGGACATCANGANGNTGTTGATGCCAAGCGTCCGTGACAAC              | 234 |
| DB                    | 82  | GGTAAATGTTTCCAAAGACATAACACACTGCTGCTAGATCTTAAAGCCTTTAAAGACACC       | 141 |
| QY                    | 235 | ATATACCATTTTGTCAAGCGGTACAGGACCAAGGATCCATCCCTGAAATAGGAGTTAA         | 294 |
| DB                    | 142 | ATTGATCTGTTTGTGAGAGGTATCGAGACATGACATCTCGTGG-TTGCAGGTATAGA          | 200 |
| QY                    | 295 | AGCTAGAGGNTCANTTTCGGACAACTANNTCTTANAANNAATTTGGTCAAAATNGTG          | 354 |
| DB                    | 201 | GGCTCGCGGTTTCATATTCGGTTCACCCA--TCGCATTAGCCATCGGACAAAATTTGTT        | 258 |
| QY                    | 355 | NCNATTGAGGAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATTTTNG            | 414 |
| DB                    | 259 | CCTCTTCGTAACCAAGAAAATTTCCCGGCCAAATATATTTCAAGAGTATGAGTTGGAG         | 318 |
| QY                    | 415 | GA 416   |     |
| DB                    | 319 | TA 320   |     |
| RESULT 9              |     |  |     |
| LOCUS                 |     | ATAPT2   |     |
| DEFINITION            |     | A.thaliana Atapt2 mRNA for adenine phosphoribosyltransferase.      |     |
| ACCESSION             |     | X96866   |     |
| VERSION               |     | X96866.1 GI:1402893  |     |
| KEYWORDS              |     | adenine phosphoribosyltransferase; Atapt2 gene.                    |     |
| SOURCE                |     | thale cress  |     |
| ORGANISM              |     | Arabidopsis thaliana   |     |
|                       |     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |     |
|                       |     | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;       |     |
|                       |     | Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.     |     |
| REFERENCE             |     | 1 (bases 1 to 727)   |     |
| AUTHORS               |     | Schnorr, K.M.  |     |

| FEATURES              |     | Location/Qualifiers  |     |
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| source                |     | 1..847   |     |
|                       |     | /organism="Arabidopsis thaliana"   |     |
|                       |     | /db_xref="taxon:3702"  |     |
|                       |     | /clone="11009"   |     |
|                       |     | 154..705   |     |
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|                       |     | 2.4.2.7)-like protein"   |     |
|                       |     | /protein_id="AA061081.1"   |     |
|                       |     | /db_xref="GI:21536749"   |     |
|                       |     | /translation="MSGNKEEDPRINGIKTKRVVDPFKKGFIMFQDITVLLDPKA  |     |
|                       |     | FKDTDLFVRYRDMNISVAGIEARGFPGPIALAIKAKEVPLRKPGLPGQIFEE   |     |
|                       |     | EYELYGNDRLEHIGAVAGDRLVDDLIATGTTCAAINLLRVAEIVVEACVIE  |     |
|                       |     | ELPELKGRLKGPCLMLVEYR"  |     |
| BASE COUNT            |     | 245 a 150 c 199 g 253 t  |     |
| ORIGIN                |     |  |     |
| Query Match           |     | 17.5%; Score 77; DB 8; Length 847;   |     |
| Best Local Similarity |     | 54.1%; Pred. No. 1.5e-07;  |     |
| Matches               |     | 160; Conservative 0; Mismatches 133; Indels 3; Gaps 2;   |     |
| QY                    | 115 | GATCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTMATNCCGACTTCCAAAGCCA  | 174 |
| DB                    | 178 | GATCTCTGATCGATGTGTATCAAAATAGATCCGTGCTCCAGATTTCCCAAGAAA   | 237 |
| QY                    | 175 | GGATNATGTTTCAGGACATCANGANGNTGTTGATGCCAAGCGTCCGTGACAAC  | 234 |
| DB                    | 238 | GGAAATATGTTTCAAGACATACACAGGTGTTGGATCCGAAGCCTTCAAAGACACA  | 297 |
| QY                    | 235 | ATATACCATTTTGTCAAGCGGTACAGGACCAAGGATCCATCCCTGAAATAGGAGTTAA   | 294 |
| DB                    | 298 | ATTGATCTGTTTGGAGAGGTACAGACAAAGACATCTCAGTGG-TTGCAGGAATAGA   | 356 |
| QY                    | 295 | AGCTAGAGGNTCANTTTCGGACAACTANNTCTTANAANNAATTTGTCRAAATNGTG   | 354 |
| DB                    | 357 | GGCTCGGTGTTTCTATTCGGTCCACCGA--TCGCGGTAGCCATTTGGAGCAAAATTTGTT   | 414 |
| QY                    | 355 | NCNATTGAGGAGCNAATNAGNTGCCANGCNAATGATTTTNGAATANGAATATT  | 410 |
| DB                    | 415 | CCTCTGCCAAACCAAGAAATACCTGCTGTAACAATATTTGAGGAATAGAGTT   | 470 |
| RESULT 8              |     |  |     |
| LOCUS                 |     | AV133689   |     |
| DEFINITION            |     | Arabidopsis thaliana clone C103141 (B) putative adenine phosphoribosyltransferase (At4g12440) mRNA, complete cds.  |     |
| ACCESSION             |     | AV133689   |     |
| VERSION               |     | AV133689.1 GI:22136607   |     |
| KEYWORDS              |     | FLI CDNA.  |     |
| SOURCE                |     | Arabidopsis thaliana.  |     |
| ORGANISM              |     | Arabidopsis thaliana   |     |
|                       |     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |     |
|                       |     | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;   |     |
|                       |     | Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.   |     |
| REFERENCE             |     | 1 (bases 1 to 579)   |     |
| AUTHORS               |     | Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A. |     |
| TITLE                 |     | Arabidopsis Open Reading Frame (ORF) Clones  |     |
| JOURNAL               |     | Unpublished  |     |
| REFERENCE             |     | 2 (bases 1 to 579)   |     |
| AUTHORS               |     | Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A. |     |
| TITLE                 |     | Direct Submission  |     |
| JOURNAL               |     | Submitted (17-JUL-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA   |     |

|                       |        |                  |       |             |
|-----------------------|--------|------------------|-------|-------------|
| Query Match           | 15.7%; | Score 69;        | DB 8; | Length 850; |
| Best Local Similarity | 50.2%; | Pred. No. 1e-05; |       |             |

| Matches 167; Conservative 0; Mismatches 163; Indels 3; Gaps 2;  |  |   |                            |
|---|--|---|----------------------------|
| Qy  | 91   | CGCGTGGTGGCGATGGCGTTCGCGCTTGGCGGNGATCGNCTCCTNCAATCCNG       | 150                        |
| Db  | 70   | CGCGTGGAGATGGTTGCGAGGAGACCCGAGATTAAAGCCATCTCCGACGCCATTCGT   | 129                        |
| Qy  | 151  | GTNATNCCGACTTNCACAGCCAGGATATGTTTCAGGACATCANGANGTNGTTC       | 210                        |
| Db  | 130  | GTCAATTCCTCATCTCCCAAGACTGGGATCATGTTTCAGGACATACAAAGTGTGCTG   | 189                        |
| Qy  | 211  | GATCCAAAGCGNCCGTCGACACATATACCATTTTCAAGCGGTACAGGACCAAGN      | 270                        |
| Db  | 190  | GATCCAGTGGCTTTAAACATGTCTCGACATCTTCGTTCATGTTACAGGACATGAAC    | 249                        |
| Qy  | 271  | ATCACNTGGAANAATAGAGTAAAGCTAGAGGNTCAANTTCGGAACAACACTANNTCTTA | 330                        |
| Db  | 250  | ATCTCTCTCG-TCGCGGAGTAGAGGCGAGGAGTATCATATTTGGACCTCCCATCGCGT- | 307                        |
| Qy  | 331  | NAANNAATGTCAAAAATNGTNCNATTCGAGGAACNNAATNAGNTGCCANGCNAAT     | 390                        |
| Db  | 308  | TAGCCATAGGTGCGAAGTTCGTTCCACTAGCCAAACCGGAAACTACCCGGGAGATG    | 366                        |
| Qy  | 391  | GATTTTNGAATANGAATTTTNGGAATNNGGA                             | 423                        |
| Db  | 367  | ATAACCGAAGACTAGCAACTTGAGTATGGAAGA                           | 399                        |
| RESULT 11   |  |   |                            |
| ATF7K2/C  |  |   |                            |
| LOCUS   | ATF7K2   | 106702 bp   | DNA linear PLN 10-MAR-2000 |
| DEFINITION  | Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSA project).  |   |                            |
| ACCESSION   | AL033345   |   |                            |
| VERSION   | AL033345.2   | GI:5738368  |                            |
| KEYWORDS  | Arabidopsis thaliana.  |   |                            |
| SOURCE  | Arabidopsis thaliana.  |   |                            |
| ORGANISM  | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  |   |                            |
| REFERENCE   | 1 (bases 1 to 16021)   |   |                            |
| AUTHORS   | Bevan,M., Robben,J., Grymonprez,B., Volckaert,G., Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  |   |                            |
| JOURNAL   | Unpublished  |   |                            |
| REFERENCE   | 2 (bases 15770 to 106702)  |   |                            |
| AUTHORS   | Bevan,M., Wedler,H., Hambutt,R., Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.   |   |                            |
| JOURNAL   | Unpublished  |   |                            |
| REFERENCE   | 3 (bases 92830 to 92989)   |   |                            |
| AUTHORS   | Bevan,M., Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.   |   |                            |
| JOURNAL   | Unpublished  |   |                            |
| REFERENCE   | 4 (bases 1 to 106702)  |   |                            |
| AUTHORS   | EU Arabidopsis sequencing project.   |   |                            |
| TITLE   | Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk |   |                            |
| COMMENT   | On Aug 18, 1999 this sequence version replaced gi:3892698. Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <a href="http://www.mips.biochem.mpg.de/proj/thal/">http://www.mips.biochem.mpg.de/proj/thal/</a> .   |   |                            |
| FEATURES  | Location/Qualifiers  |   |                            |
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|   | /variety="Columbia"  |   |                            |
|   | /db_xref="taxon:3702"  |   |                            |
|   | /chromosome="4"  |   |                            |
| misc_feature  | 1. .15769  |   |                            |
|   | /note="basepairs 1-15769 are not integral part of BAC"   |   |                            |
| clone F7K2"   |  |   |                            |
| 3. .821   |  |   |                            |
| /gene="AT4g22380"   |  |   |                            |
| complement(join(3. .98,594. .821))  |  |   |                            |
| /gene="AT4g22380"   |  |   |                            |
| complement(join(<3. .98,594. .821))   |  |   |                            |
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| /note="strong similarity to NHP2/RS6 FAMILY PROTEIN, Homo sapiens, PID:g4826860   |  |   |                            |
| contains Ribosomal protein L7Ae signature AA73-90   |  |   |                            |
| contains EST gb:F13981"   |  |   |                            |
| /codon_start=1  |  |   |                            |
| /product="Ribosomal protein L7Ae-like (fragment)"   |  |   |                            |
| /protein_id="CAB52812.1"  |  |   |                            |
| /db_xref="GI:5738369"   |  |   |                            |
| /translation="MTGEVVPNPKAYPLADSLISITIMDLVOQATNYKOLKKGANEATK TLRGISEFVMAADAEPIELLHLPLAEDKNVPYFVPSKQALGRACGVTRPIAC SVTSNE"  |  |   |                            |
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| complement(99. .593)  |  |   |                            |
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| complement(594. .821)   |  |   |                            |
| /gene="AT4g22380"   |  |   |                            |
| /number=2   |  |   |                            |
| 1789. .2973   |  |   |                            |
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| complement(1789. .2973)   |  |   |                            |
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| complement(1789. .2973)   |  |   |                            |
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| /note="similarity to various predicted proteins, Arabidopsis thaliana"  |  |   |                            |
| /codon_start=1  |  |   |                            |
| /product="putative protein"   |  |   |                            |
| /protein_id="CAB52813.1"  |  |   |                            |
| /db_xref="GI:5738370"   |  |   |                            |
| /translation="MAECPDLDLINEMFLRLRATLTKRVLSKPCFSLIDSPFVSSH NSPVDLAFNPSTKRLHRLPIEDIDFERDITREYVYGLVSDYDDDFKVVRIVOCK LKEGKKFPCPVEVKVFSLKNSKRVCLMFEQILMISYVHLLPRGCVVNNHL HWILPRQGVAFNAIILDLASDDIGVLSFFQELIENMDIGVLDGCYCLMCYDEY SHVDVWLKIEDYKSWTKLYRVPKPEVESVEFHPLCSKDRSKILLEINNAANLL WFDLESQSLATAGIECDSSPTADILVSSLVLCCKGDPDQAQRSKDKMMPKSTRWYA LL"   |  |   |                            |
| complement(1789. .2973)   |  |   |                            |
| /gene="AT4g22390"   |  |   |                            |
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| 4728. .5711   |  |   |                            |
| /gene="AT4g22400"   |  |   |                            |
| 4728. .5711   |  |   |                            |
| /gene="AT4g22400"   |  |   |                            |
| /note="similarity to various predicted proteins, Arabidopsis thaliana"  |  |   |                            |
| contains EST gb:Z17595"   |  |   |                            |
| /codon_start=1  |  |   |                            |
| /product="putative protein"   |  |   |                            |
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| /db_xref="GI:5738371"   |  |   |                            |
| /translation="MLSSHLSQICFCSCRDPLGNLPADLIRKCTDLMDLNFAGQRRLT LNKWKIALDPSFRKAGYREERWLLYRERGSGTREFDPVRRVHRGNDPRLADARFL GSTLGLWMSSELDLNPRTKHTQFLYNPFISEIQQLPETLDSPTGVLKRVGLITGN PSDNNTYACLITDYLHGNRRDTYLLIYVAKTSGRWFONMSVASMLVWGIFDTWY TESISPSDKISIEIWPGRYDFTFQGEWNSNFIIPVDPTQWDPFDQSLYHVKHRLQ LPENPSTLAIITGTSTDRTRVRNKLIGDQSDDDPRASDHIIDGVVWEVRP" |  |   |                            |
| 4728. .5711   |  |   |                            |
| /gene="AT4g22400"   |  |   |                            |
| /number=1   |  |   |                            |
| 6112. .8034   |  |   |                            |
| /gene="AT4g22410"   |  |   |                            |
| complement(join(6112. .6297,6675. .6812,6908. .7075,  |  |   |                            |

7168. 7353.7429. .7513,7775. .8034))  
/gene="At4g22410"  
complement(6112. .6297,6675. .6812,6908. .7075,  
7168. 7353.7429. .7513,7775. .8034))  
/gene="At4g22410"  
/note="similarity to snRNP assembly factor like protein,  
Homo sapiens, PID:q5730025"  
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/db\_xref="GI:5738372"  
/translation="MVFEQVDFHFFERFCVSLSNLNVYACLVCGKYQGRSQKSHAY  
THSLEAHGVYIMLLEKTYICUPDSYEINDPSLDDIRHVLNFRFRAQVNEUDKNROW  
SRALDSGLYPLGMVNIQKTEFYVNTIQSLMRVTPLENFHIFENYOHKSPPLVHC  
FGELTRKIHARFKQVSPHEFLQAVMKASRFRFGQSDPVEFMSKLLNLTLMOL  
RTSKDASSIIFHKFCQLELVKFEFQGNENKEISRMFSLMLGLDLPPLPLFKDVMKNI  
IPOVALFDLLKFKDGETVEVVRPKLARMYRIKSPRYLMFHMVREKKNFFKPKNP  
TLGESV"  
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/number=2  
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/number=2  
complement(6908. .7075)  
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/gene="At4g22410"  
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complement(7354. .7428)  
/gene="At4g22410"  
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/number=5  
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/number=5  
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8059. .8449  
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8450. .13234  
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13234. .13624  
/note="389bp LTR"  
13513. .14331  
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complement(join(13513. .13618,13701. .14033,14216. .14331))  
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thaliana  
contains EST gb:T44427"  
/codon\_start=1  
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/protein\_id="CAB52816.1"  
/db\_xref="GI:5738373"  
/translation="MACEPTDLNEMFLRLRATLTKKRVLSKPCESLIDSPKRVIE  
RSDSPPLGPNHLLPLANAYDDDEEGNELKKSQARRNGVAKGEGNGKNVNGAQ  
EVDDEDDDDASKRGKHSRHEVRDCCFYLDVTNRQVIIDQFLMLRVLATMRK

RMRTGGRKAKAMEKYLKVLKSGS"  
complement(13513. .13618)  
/gene="At4g22420"  
/number=1  
complement(13619. .13700)  
/gene="At4g22420"  
/number=1  
complement(13701. .14033)  
/gene="At4g22420"  
/number=2

Query Match 11.98; Score 52.2; DB 8; Length 106702;  
Best Local Similarity 63.78; Pred. No. 0.18; Indels 0; Gaps 0;  
Matches 72; Conservative 0; Mismatches 41;

QY 168 AAAGCCAGGATATGTTCAGGACATCANGANGTGTTCGATCCCAAGCGNCCG 227  
II IIII II IIII IIII II IIII IIII IIII IIII IIII IIII IIII  
DB 72738 AATTCAGGATATGTTCAGGACATCAACACAGTGTTCGATCCGAAACCTTCAA 72679

QY 228 TGACAACATATACCATTTTTCAGCGGTACAGGACCAAGGNATCACCTGG 280  
IIII II II IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 72678 AGACACAATTCATCTGTTGTGGAGAGGTACAGAGACAAGACATCTCAGTGG 72626

RESULT 12  
ATCHRIV57/c  
LOCUS ATCHRIV57 199577 bp DNA linear PLN 16-MAR-2000  
DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57.  
ACCESSION AL161557  
VERSION AL161557.2 GI:7269071  
KEYWORDS Arabidopsis thaliana.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 - (bases 48809 to 54829)  
Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and  
Mayer,K.F.X.  
Unpublished  
2 (bases 64578 to 155510)  
Wedler,H., Wambutt,R., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
Unpublished  
3 (bases 141638 to 141797)  
Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W.,  
Lemcke,K. and Mayer,K.F.X.  
Unpublished  
4 (bases 143670 to 199577)  
Hilbert,H., Braun,M., Holzer,E., Brandt,A., Duesterhoeft,A.,  
Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
Unpublished  
5 (bases 1 to 199577)  
EU Arabidopsis sequencing project.  
Direct Submission  
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer  
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG. E-mail:  
lemcke@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de Project  
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge  
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,  
E-mail: michael.bevan@bbsrc.ac.uk  
Information on performance of analysis and a more detailed  
annotation of this entry and other sequences of chromosomes 3, 4  
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/lhal/>  
This fragment has an overlap with ATCHRIV56 at the 5' end and an  
overlap with ATCHRIV58 at the 3' end.

FEATURES  
Location/Qualifiers  
1..199577  
/organism="Arabidopsis thaliana"  
/variety="Columbia"  
/db\_xref="taxon:3702"  
/chromosome="4"  
6674..9057  
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source  
gene

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7667..7775,7863..7978,8361..8454,8588..8777,8909..9057))
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7667..7775,7863..7978,8361..8454,8588..8777,8909..9057))
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/feature="similarity to alternative oxidase, Mangifera
indica, PIR:S45035
contains EST gb:T42793, AI994896.1, AI997645.1, R30022,
AA395166"
/codon_start=1
/product="putative protein"
/protein_id="CAB79181.1"
/db_xref="GI:7269072"
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RRLLRNRHVQATILQDDERKVVVEESFKAETGTGTEEPNNSSSTSAFETWII
KLEQGVNFTDSVTKILDLYDRDYARFVLETIARVPYAFAMSVLHMYETGWMR
RADYLAHFAESNEMHLLIMEELGGNSWDFRLAQIATFYFMTVFVLYILSPRM
AYHFSQVSHAYETVDKELKASGEELNMPADIAVKVYTGDDLFLFENLYDVFNII
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exon      complement(6674..6882)
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intron    complement(6883..7267)
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exon      complement(7268..7339)
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exon      complement(8588..8777)
/feature="AT4g22260"
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exon      complement(8909..9057)
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CDS      join(10103..10244,10395..10516,11327..11779,11868..12174,
12254..12393)
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/feature="contains EST gb:AI997575.1"
/codon_start=1
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SNEGTSFYSLWSISWKRFRFLFDLKLMDVSDKRVIEAEIQRSKLRLMIFVLSL
TFEATYRWIISGFIQNPYIINPILSHVACTQLQSSWLYRNSLFIIVCILKITCH
LOTLLDDFARCFSEITDVSALGEHOKIRRNLRIVSHRFRFILLSLVLTATQFM
ALLTTTRASVAVNIVEGELALCSLSLVTGVFICRSATKITHKAQSVTLAAKWNVC
AYVDSFDHLDGETPTGSIIQSQSLRGNAIETSDDEGEQDDDLNTKIHIYANTIS
YKRALVTYLLNNKAGITVYGVFLVDRSWLNTIFGIELALLLLLNKNTIGILA"
10103..10244
/feature="AT4g22270"
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intron    10245..10394
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exon      10395..10516
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/feature="codon recognized: GUA"
11327..11779
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11868..12174
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12254..12393
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14209..14314,14995..15111))
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/feature="similarity to hypothetical protein, chr.4,
Arabidopsis thaliana, PATCH:G2392763
contains EST gb:AI998861.1, AI9993240.1"
/codon_start=1
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/protein_id="CAB79183.1"
/db_xref="GI:7269074"
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FGVVDAGDLLFRITPERFIRIWMRDRINEATSVLSMRWRIYLFARPNLCDDQE
VGGDSFIDFVDRVLTQVTFPIRISIKRMSIDTGHVTRMWDVLEHGVSLDDIDI
ISEDIGFVPLEITFCTKLVELKLARGFAMYPDVYVSLPSTLFLSSIFWNCDDCP
LGRLLSACPVLEELTITGGCWOHIEFCRTVSSSTLKLITSSFHYEWGITIDTPSL
AYLEYSDLVPRHFFPNVLSLVEAKLALDCSDSNPTNLKGLRNVVELELSSGYTSQ
ILYDFRAIPVLSKFLRSLKSNRHYIWNLLPILLESKPLETVIKGPLSADRYE
REYGLSCPVKVLEITEYGGKYELEQNEHFLKLPLCLELVKVRASAINDKESRTKD
LLMVPRSSNCKILKFC"
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/feature="AT4g22280"
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/feature="AT4g22280"
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/number=2
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/number=2
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/gene="AT4g22280"
/number=3

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Best Local Similarity 63.7%; Pred. No. 0.19;
Matches 72; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 168 AAGCCAGGATATTTTCAGGACATCANGANGTGTTCGATCCCAAGCGGTCGG 227
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121546 AATTCAGGAATATGTTTCAGACATACACACAGTGTGTTCGATCCCAAGCGTTCNA 121487
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 228 TGACAACATATACCATTTGTCAAGCGGTACAGGACCAAGGNATCACCNTGG 280
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121486 AGACAAATTCATGCTGTTGTGGAGAGGTACAGAGACAAGAACATCTCASTGG 121434
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RESULT 13
AP004523/c      86209 bp      DNA      linear      PLN 14-DEC-2001
LOCUS      Lotus japonicus genomic DNA, chromosome 1, clone:LJT03J05, TM0050,
DEFINITION      complete sequence.
ACCESSION      AP004523
VERSION      AP004523.1 GI:17736890
KEYWORDS      HTG.
SOURCE      Lotus japonicus DNA, clone_lib:LJT library clone:LJT03J05.
ORGANISM      Lotus japonicus
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
      Lotus.

REFERENCE
1 Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S.
  Structural Analysis of a Lotus japonicus Genome. I. Sequence
  Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb
  Regions of the Genome
  Unpublished
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 86209)
AUTHORS      Nakamura,Y.
TITLE      Direct Submission
JOURNAL      Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research
      Institute, Department of Plant Gene Research; 1532-3, Yana,
      Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
      URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
      Fax:81-438-52-3934)
FEATURES
source      Location/Qualifiers
1 . 86209
   /organism="Lotus japonicus"
   /db_xref="taxon:34305"
   /chromosome="1"
   /clone="LJT03J05"
   /clone_lib="LJT library"
   /note="TAC clone:TM0050"
BASE COUNT   28052 a 16513 c 15191 g 26453 t
ORIGIN

Query Match      11.6%; Score 51.2; DB 8; Length 86209;
Best Local Similarity 51.6%; Pred. No. 0.29;
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

OY 97 GTGGGATGGGTCGTGATGCGGCTGGCGGNGATCGNCCTTCATCCNGGTAATN 156
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15980 GTTGTGATGGTGGTTGTTATATGATTTCATTCGATTCGTTGTTGGAATTGA 15921
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 157 CCCGACTTNCACAGCCAGGATATGTTTCAGGACATCANGANGTGTTCGATCCC 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15920 ATTGTGTTGCCATATCAGGTATCATGTCCAGGATATACCACTCTGCTTCGATCCC 15861
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 217 AAGCGGTCGCTGACACATATACCATTTGTCAAGCGGTACAGGACCAAGGNATCACC 276
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15860 AAGGCTTCAAGGATACCATTCGACTTGTTGTTGAGAGGTACAGAGATCAAAACATTCT 15801
OY 277 NTGS 280
Db 15800 GTTG 15797

CNS08CAA      132914 bp      DNA      linear      HTG 10-JUL-2002
LOCUS      Oryza sativa chromosome 12 clone OSJNBa0010M16, *** SEQUENCING IN
DEFINITION      PROGRESS ***, 8 ordered pieces..
ACCESSION      AL831797
VERSION      AL831797.1 GI:21732215
KEYWORDS      HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE      Oryza sativa.
ORGANISM      Oryza sativa
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
      Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 132914)
AUTHORS      Choinsie,N., Orjeda,G., Cattolico,L., Demange,N., Wincker,P.,
      Segurens,B., Pelletier,F., Scarpelli,C., Salanoubat,M.,
      Weissenbach,J. and Quetier,F.
      Oryza sativa chromosome 12 sequencing
      Unpublished
      Genoscope.
      Direct Submission
      Submitted (09-JUL-2002) Genoscope - Centre National de Sequencage :
      BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
      - Web : www.genoscope.cns.fr)
      IMPORTANT: This sequence is unfinished and does not necessarily
      represent the correct sequence.
      Work on the sequence is in progress and the release of this data is
      based on the understanding that the sequence may change as work
      continue. The sequence may be contaminated with foreign sequence
      from E.coli, yeast, vector, phage, etc.
      Contigs composition :
      27738 bp contig from 1 to 27738
      5061 bp contig from 27839 to 32899
      21353 bp contig from 33000 to 54352
      53531 bp contig from 54453 to 107983
      11624 bp contig from 108084 to 119707
      4526 bp contig from 119808 to 125333
      4861 bp contig from 125434 to 130294
      2520 bp contig from 130395 to 132914.
      * NOTE: This is a 'working draft' sequence. It currently
      * consists of 8 contigs. Gaps between the contigs
      * are represented as runs of N. The order of the pieces
      * is believed to be correct as given, however the sizes
      * of the gaps between them are based on estimates that have
      * provided by the submittor.
      * This sequence will be replaced
      * by the finished sequence as soon as it is available and
      * the accession number will be preserved.
      * 1 27738: contig of 27738 bp in length
      * 27739 27838: gap of 100 bp
      * 27839 32899: contig of 5061 bp in length
      * 32900 32999: gap of 100 bp
      * 33000 54352: contig of 21353 bp in length
      * 54353 54452: gap of 100 bp
      * 54453 107983: contig of 53531 bp in length
      * 107984 108083: gap of 100 bp
      * 108084 119707: contig of 11624 bp in length
      * 119708 119807: gap of 100 bp
      * 119808 125333: contig of 5526 bp in length
      * 125334 125433: gap of 100 bp
      * 125434 130294: contig of 4861 bp in length
      * 130295 130394: gap of 100 bp
      * 130395 132914: contig of 2520 bp in length.
      Location/Qualifiers

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gene 3834..4436
CDS   /gene="VC1056"
      /db_xref="GI:9655522"
      /note="similar to GB:M38777 SP:P12727 GB:X15761 PID:145299
      PID:42697; identified by sequence similarity; putative"
      /codon_start=1
      /transl_table=11
      /product="recombination protein RecR"
      /protein_id="AAF94215.1"
      /db_xref="GI:9655522"
      /translation="MRTSHMLEALRCLPGVGPQSAQMAFHLLQDRKGGQLQIA
      EALSQAMVIGHCQCRTEQDVCHICSNPKRKGOLCVVESPADIAALEAGQFS
      GRVFLMGLHSGDIPGSDIGDITLDYRLQDGISEVILATNPTEGEATAQYIAEL
      CRHQVTASRIAHGVPGVGELELDVDTLSSHLLGRHKL"
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      PID:1945383 PID:1945451; identified by sequence
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      /transl_table=11
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      /protein_id="AAF94216.1"
      /db_xref="GI:9655523"
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      LGVLSFDQIGESDFEVQVNVKQAQFLMTQALLPLHKSADARIVFTTSTVGHIGRA
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      PID:1742067; identified by sequence similarity; putative"
      /codon_start=1
      /transl_table=11
      /product="soxB protein, peptidase U7 family"
      /protein_id="AAF94219.1"
      /db_xref="GI:9655526"
      /translation="MSHLEFLDLYGLFLAKIVTVVVALVAVLVIVKSLGGSGGAKGE
      LEITDTEHQHKEVERLEYLHDEAPLKARDKKKEKAKSKRSKQAAKEGEL
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ASSQLDLKKAAGLPLTIAVDKVAASGGYMMACIADKIVSAPFAIVSGSIGVVAQLPNFH
KLLKKNDFEQCTAGAYKRLTFMGENTDKAREKFQOELEETHQLFKDFIREHRPAL
DLDKRVATGEHWFCTQAKALGLVDRIQTSDDLIVAACKSKTVLLRLRYTQKKLADKLAG
VAGDAADNVLLKLLISRGORPLV"
complement(7551..8618)
/gene="VC1061"
complement(7551..8618)
/gene="VC1061"
/note="similar to GB:AL123456; identified by sequence
similarity; putative"
/codon_start=1

Query Match      11.4%; Score 50.2; DB 1; Length 10172;
Best Local Similarity 55.0%; Pred. No. 0.35;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 132 GATCGNCTCTTCATCCNGGTNATCCCGACTTNCCTCAAGCCAGGATNATGTTTCAGGA 191
Db 800 GATCAAAATCCAGCATCAAAAGTATTCTTGACTACCCGAAAGGCAFTCTGTTTCGTGA 859
QY 192 CATCANGANGTGTGTTGATCCCAAGCGTCCGTGACACACATATACCATTTTGTCAA 251
Db 860 TGTGACCAGCTTCTGGAAGATGCCCAAGCCTACCAAGCGACCATTCACACTTCTGTTGA 919
QY 252 GCGGTACAGGACCAAGGNATCACCTGG 280
Db 920 AAAGTACAAAGACATGGGTTTACCAGG 948

Search completed: November 30, 2002, 05:56:47
Job time : 2954 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 02:41:07 ; Search time 52 seconds  
(without alignments)  
2594.957 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440

Sequence: 1 cgtccgcgcgcgcgacttc.....ggaaatnntagataaaaaant 440

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

#### Database :

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length  | ID                | Description        |
|------------|-------|-------------|---------|-------------------|--------------------|
| 1          | 86.6  | 19.7        | 729     | US-08-447-010-1   | Sequence 1, Appli  |
| 2          | 36.8  | 8.4         | 4403765 | US-09-103-840A-2  | Sequence 2, Appli  |
| 3          | 35.2  | 8.0         | 4411529 | US-09-103-840A-1  | Sequence 1, Appli  |
| 4          | 35    | 8.0         | 4403765 | US-09-103-840A-2  | Sequence 2, Appli  |
| 5          | 35    | 8.0         | 4411529 | US-09-103-840A-1  | Sequence 1, Appli  |
| 6          | 34.8  | 7.9         | 3441    | US-08-525-864A-1  | Sequence 1, Appli  |
| 7          | 34.4  | 7.8         | 419     | US-08-519-777-30  | Sequence 30, Appli |
| 8          | 34.4  | 7.8         | 419     | US-08-742-035-30  | Sequence 30, Appli |
| 9          | 34.4  | 7.8         | 419     | US-08-777-019-30  | Sequence 30, Appli |
| 10         | 34.4  | 7.8         | 419     | US-08-777-143-30  | Sequence 30, Appli |
| 11         | 34.4  | 7.8         | 419     | US-08-775-414-30  | Sequence 30, Appli |
| 12         | 34.4  | 7.8         | 419     | US-08-931-858E-30 | Sequence 30, Appli |
| 13         | 34.4  | 7.8         | 419     | US-08-981-739-30  | Sequence 30, Appli |
| 14         | 34.4  | 7.8         | 419     | US-09-128-026-30  | Sequence 30, Appli |
| 15         | 34.4  | 7.8         | 426     | US-08-775-414-88  | Sequence 88, Appli |
| 16         | 34.4  | 7.8         | 450     | US-08-775-414-90  | Sequence 90, Appli |
| 17         | 34.4  | 7.8         | 585     | US-08-519-777-12  | Sequence 12, Appli |
| 18         | 34.4  | 7.8         | 585     | US-08-742-035-12  | Sequence 12, Appli |
| 19         | 34.4  | 7.8         | 585     | US-08-777-019-12  | Sequence 12, Appli |
| 20         | 34.4  | 7.8         | 585     | US-08-777-143-12  | Sequence 12, Appli |
| 21         | 34.4  | 7.8         | 585     | US-08-775-414-12  | Sequence 12, Appli |
| 22         | 34.4  | 7.8         | 585     | US-08-931-858E-12 | Sequence 12, Appli |
| 23         | 34.4  | 7.8         | 585     | US-08-981-739-12  | Sequence 12, Appli |
| 24         | 34.4  | 7.8         | 585     | US-09-128-026-12  | Sequence 12, Appli |
| 25         | 34.4  | 7.8         | 1023    | US-08-931-858E-49 | Sequence 49, Appli |
| 26         | 34.4  | 7.8         | 1028    | US-08-118-200-1   | Sequence 1, Appli  |
| 27         | 34.4  | 7.8         | 1028    | US-08-458-745-1   | Sequence 1, Appli  |

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C 31 33.8 7.7 4257 4 US-09-259-821A-1  
C 32 33.8 7.7 4257 4 US-08-843-659-1  
C 33 33.8 7.7 12001 1 US-08-458-568A-11  
C 34 33.4 7.6 306 3 US-08-775-414-86  
C 35 33.4 7.6 618 2 US-08-900-751-3  
C 36 33.4 7.6 618 2 US-08-900-818-3  
C 37 33.4 7.6 3919 2 US-08-866-650-4  
C 38 33.4 7.6 3919 2 US-09-021-287-4  
C 39 33.4 7.6 3919 4 US-09-240-473-4  
C 40 33.2 7.5 2467 3 US-08-753-007A-1  
C 41 33.2 7.5 2467 3 US-09-398-496-1  
C 42 33 7.5 300 1 US-08-519-777-10  
C 43 33 7.5 300 1 US-08-742-035-10  
C 44 33 7.5 300 1 US-08-777-019-10  
C 45 33 7.5 300 2 US-08-777-143-10

#### ALIGNMENTS

RESULT 1  
US-08-447-010-1  
; Sequence 1, Application US/08447010  
; Patent No. 5770718  
; GENERAL INFORMATION:  
; APPLICANT: MOFFATT, BARBARA  
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 330 University Avenue, Suite 701  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/447.010  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/230,695  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,132  
; FILING DATE: 26-MAY-1992  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, MICHAEL I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1811-183 MTS:vg  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; TELEX: 065-24567 SIMBAS  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(18..569)

Sequence 133, Appl  
Sequence 14, Appl  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 11, Appl  
Sequence 86, Appl  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 1, Appli  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 10, Appl

[REDACTED]

[REDACTED]





| Query Match           | 7.8%  | Score 34.4     | DB 1     | Length 419 |
|-----------------------|---|----------------|----------|------------|
| Best Local Similarity | 47.0%   | Pred. No. 0.87 |          |            |
| Matches 86            | Conservative 0  | Mismatches 97  | Indels 0 | Gaps       |
| Qy 1                  | CGTCGGCGCGCGGCGACTTCGCGCTTTTCGTCGCCGCGTCAGCGTCGCGGCTCCNNTGAGC | 60             |          |            |
| Db                    |   |                |          |            |
| Db 105                | CGCGGGCGCGCGCGGGGCTTCGGCCTTGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGC   | 164            |          |            |
| Qy 61                 | GTGCGCGTCAACCGCGCGCAGGCGAGCGCGGTGTGGCGCATGCGTCNCGCTGATGCG     | 120            |          |            |
| Db 165                | GAGCTGGGCGCTGGGCTACACGTCGGATGAGACCGTGCTGTTCGCTACTCGCGCAGGCGCG | 224            |          |            |
| Qy 121                | CGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCGAAGCCAGGAGTN   | 180            |          |            |
| Db 225                | TGCAGGCGGCCATCCGCATCTAGACCTGGGCGCTTGGCGCCTGGCGCCAGCGGAGCGCG   | 284            |          |            |
| Qy 181                | ATG 183   |                |          |            |
| Db 285                | GTG 287   |                |          |            |

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RESULT 10
US-08-777-143-30
; Sequence 30, Application US/08777143
; Patent No. 5843914
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,143
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-777-143-30

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Query Match 7.8%; Score 34.4; DB 2; Length 419;  
 Best Local Similarity 47.0%; Pred. No. 0.87;  
 Matches 86; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
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Db      165  GAGCTGGGCGCTGGGCTACACCTCGGATGAGACCGTGTCTGTTCGCTACTCGCAGGCGCG 224
QY      121  CGCTTGGCGGAGTGCNCTCCTTCGATCCGCTGATCCGCTGATCCGCTGATCCGCTGATCCG 180
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QY      181  ATG 183
Db      285  GTG 287

RESULT 11
US-08-775-414-30
; Sequence 30, Application US/08775414
; Patent No. 6090778
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,414
; FILING DATE: 31-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965805
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-775-414-30

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|-----------------------|--------------|----------------|---------------|------------|
| Query Match           | 7.8%         | Score 34.4     | DB 3          | Length 419 |
| Best Local Similarity | 47.0%        | Pred. No. 0.87 |               |            |
| Matches 86            | Conservative | 0              | Mismatches 97 | Indels 0   |
|                       | Gaps         | 0              |               |            |

QY 121 CGCTTGGCGGATCGNCTCCTNCATCCNCGGTNATCCCGACTTNCCAAAGCCAGGGATN 180











## RESULT 2

US-09-770-445-347  
; Sequence 347, Application US/09770445  
; Patent No. US2002023281A1

; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jorn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kriker, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; TITLE OF INVENTION: thaliana

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09770,445

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 347

; LENGTH: 945

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(945)

; OTHER INFORMATION: n = A,T,C or G

US-09-770-445-347

Query Match 14.5%; Score 63.8; DB 10; Length 945;

Best Local Similarity 61.4%; Pred. No. 5.3e-10;

Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 136 GNCCTTCATCCCGGTTNCCGACCTTCCAAAGCCAGGATNATGTTTCAGGACATC 195

DB 2 GCGCTTCATAGATCATCCCGACTTCCTTAACCAAGGATCATGTTTCAGGACATA 61

QY 196 ANGANNGTNTGTTGGATCCCAAGCGGNTCCGTCGACAAACATATACCAATTTTGTCAAGCGG 255

DB 62 ACGAGCTTCTTCGACACTGAGCGCTTTAAGGATCTATTGCTTTGTTGTGATAGA 121

QY 256 TACAAGGACCAAGGATCAACCTCG 280

DB 122 TACAAGATTAAGGCATATCTGTTG 146

RESULT 3

US-09-878-574-13031

; Sequence 13031, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 13031

; LENGTH: 272

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 701066549H1

US-09-878-574-13031

Query Match 13.1%; Score 57.6; DB 10; Length 272;

Best Local Similarity 71.7%; Pred. No. 2.1e-08;

Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 115 GATGGCGCTTGGCGNGATCGNCTCTCNATCCNGTATNCCCGACTTNCAGAGCCA 174

DB 179 GACAGCGCTTAGCGAGANTCGCTCTGCAATCCGAGTCATCCCGAGCTTTCCTAAGCCA 238

QY 175 GGGATNATGTTTTCAGGACATCANGANTGNT 206

DB 239 GGAATTTTTCAGGACATAACCCGCTGCT 270

RESULT 4

US-09-878-574-6826

; Sequence 6826, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 6826

; LENGTH: 269

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 701099058H1

US-09-878-574-6826

Query Match 9.4%; Score 41.4; DB 10; Length 269;

Best Local Similarity 52.8%; Pred. No. 0.002;

Matches 121; Conservative 0; Mismatches 104; Indels 4; Gaps 3;

QY 209 TCGATCCCAAGCGNTCCGTGACAAACATATACCAATTTTGTCAAGCGGTACAGGACCAAG 268

DB 1 TTGATACAAAGCGTTTCAAGACACACCGTGTGCTTTGTTGAGAGGTACAGAGATCAA 60

QY 269 GNATCACCNTGAAANTAGGAGTTAAAGCTAGAGGNTCANTTTTCGGAACAACATNNTCT 328

DB 61 ACATCAATGTTG-TCCGAGGAGTTGAAGCAAGGGCTTTATATTGTCACCCATTGC- 118

QY 329 TANAANNAATTTGTCAAAAATNGGTGNCNATTTAGGAGCNCNATNAGTNGCCANGCNA 388

DB 119 -ATTAGCTATTGGAGCAAAATTTGTCCCA-TGAGGAACCAACCAATAAATTTGCTGGGAG 176

QY 389 ATGATTTTNGAATANGAATTTTNGGAATNNGCAATNNTGATATAAAA 437

DB 177 GTATCTCAGAGAGATATTCTTTGGAGTATGGAACACACAAATGGAGA 225

RESULT 5

US-09-712-363-28

; Sequence 28, Application US/09712363

; Patent No. US20020164588A1

GENERAL INFORMATION:  
APPLICANT: Eisenberg, David  
APPLICANT: Rotstein, Sergio H.  
APPLICANT: Marcotte, Edward M.  
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
FILE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS  
FILE REFERENCE: 07419-032001  
CURRENT APPLICATION NUMBER: US/09/712,363  
CURRENT FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: PCT/US00/02246  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/179,531  
PRIOR FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: 60/117,844  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/118,206  
PRIOR FILING DATE: 1999-02-01  
PRIOR APPLICATION NUMBER: 60/126,593  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/134,093  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/134,092  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/165,124  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/165,086  
PRIOR FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-28

Query Match 8.0%; Score 35; DB 9; Length 888;  
Best Local Similarity 47.1%; Pred. No. 0.38;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGGCTCCNNTGAGCGTGTGCGGTACCGCGCGCAGGCGAGGCGGTGGTGGCG 102  
DB 106 GTGGCGGAGCGGATCCCGATCGCCCACTACCTGGCGCAGACCTATTCGGTGTGGTG 165  
QY 103 ATGGCGTNCCTGATGCGCGGTGGCGGNGATCGNCTCCTNCATCCNGGNTGATNCCCGAC 162  
DB 166 ACCTCGCGCGCGCGCGGTGGAGAACCGGACGCTTCGTCGTCGCGCGGTCAAAACGACCC 225  
QY 163 TTNCCAAAGCCAGGATGATGTTTCAGGACATCANGANGNTGNTGTCGA 212  
DB 226 GACGTGAGCCGCGTATCGCGGATCTGGCGAACCGGACTGCGCGCGGCCGA 275

RESULT 6  
US-09-726-397A-4  
Sequence 4, Application US/09726397A  
Patent No. US20020142011A1  
GENERAL INFORMATION:  
APPLICANT: PARISH, TANYA  
APPLICANT: SMITH, DEBBIE  
TITLE OF INVENTION: VACCINE  
FILE REFERENCE: 117-329  
CURRENT APPLICATION NUMBER: US/09/726,397A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 0014845.20  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 888  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
US-09-726-397A-4

Query Match 8.0%; Score 35; DB 10; Length 888;  
Best Local Similarity 47.1%; Pred. No. 0.38;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGGCTCCNNTGAGCGTGTGCGGTACCGCGCGCAGGCGAGGCGGTGGTGGCG 102  
DB 106 GTGGCGGAGCGGATCCCGATCGCCCACTACCTGGCGCAGACCTATTCGGTGTGGTG 165  
QY 103 ATGGCGTNCCTGATGCGCGGTGGCGGNGATCGNCTCCTNCATCCNGGNTGATNCCCGAC 162  
DB 166 ACCTCGCGCGCGCGGTGGAGAACCGGACGCTTCGTCGTCGCGCGGTCAAAACGACCC 225  
QY 163 TTNCCAAAGCCAGGATGATGTTTCAGGACATCANGANGNTGNTGTCGA 212  
DB 226 GACGTGAGCCGCGTATCGCGGATCTGGCGAACCGGACTGCGCGCGGCCGA 275

RESULT 7  
US-09-726-397A-2  
Sequence 2, Application US/09726397A  
Patent No. US20020142011A1  
GENERAL INFORMATION:  
APPLICANT: PARISH, TANYA  
APPLICANT: SMITH, DEBBIE  
TITLE OF INVENTION: VACCINE  
FILE REFERENCE: 117-329  
CURRENT APPLICATION NUMBER: US/09/726,397A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 0014845.20  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 2209  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
NAME/KEY: misc.feature  
LOCATION: (434)...(439)  
OTHER INFORMATION: unknown  
NAME/KEY: misc.feature  
LOCATION: (452)...(704)  
OTHER INFORMATION: unknown  
US-09-726-397A-2

Query Match 8.0%; Score 35; DB 10; Length 2209;  
Best Local Similarity 47.1%; Pred. No. 0.64;  
Matches 80; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 43 GTCCGGGCTCCNNTGAGCGTGTGCGGTACCGCGCGCAGGCGAGGCGGTGGTGGCG 102  
DB 106 GTGGCGGAGCGGATCCCGATCGCCCACTACCTGGCGCAGACCTATTCGGTGTGGTG 165  
QY 103 ATGGCGTNCCTGATGCGCGGTGGCGGNGATCGNCTCCTNCATCCNGGNTGATNCCCGAC 162  
DB 166 ACCTCGCGCGCGCGGTGGAGAACCGGACGCTTCGTCGTCGCGCGGTCAAAACGACCC 225  
QY 163 TTNCCAAAGCCAGGATGATGTTTCAGGACATCANGANGNTGNTGTCGA 212  
DB 226 GACGTGAGCCGCGTATCGCGGATCTGGCGAACCGGACTGCGCGCGGCCGA 275

RESULT 8  
US-09-815-242-7814  
Sequence 7814, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.

|    | Query Match           | 7.6%   | Score 33.6;        | DB 10;    | Length 465; |
|----|-----------------------|--|--------------------|-----------|-------------|
|    | Best Local Similarity | 42.3%  | Pred. No. 0.69;    |           |             |
|    | Matches 93;           | Conservative   | 0; Mismatches 127; | Indels 0; | Gaps        |
| QY | 218                   | AGCGNTCCGTCGACACATATACCATTTTGTCAAGCGGTACAAGGACCAAGNATCACCN     | 277                |           |             |
| Db | 444                   | AGTTGAAACCTGAAATTTCCACCATTTCTAGTTTAAACAAATAGTAGCATGGAACATAAA   | 385                |           |             |
| QY | 278                   | TGGAANATGAGCATTAAAGCTACAGGGNTCANTTTCGGAACAACATANNCTTANANNA     | 337                |           |             |
| Db | 384                   | AAATCTACACCATCTCAAGTTTACAGACTTTATTTTCAGAAAATAATGCTCTTTGGGAAGAA | 325                |           |             |
| QY | 338                   | TTGGTCAAAAATNGGTGNCNATTTGAGGAAGCNAATNAGNTGCCANGCNAATAATGATTTTN | 397                |           |             |
| Db | 324                   | TAACTCAAAAATGCTTTAAATTAATTTATTTATTTTAAAAAATACAATTGCTATTTC      | 265                |           |             |
| QY | 398                   | ANGAATANGAAATTTTNGGAATNNGGAATNNTAGATAAAAA                      | 437                |           |             |

Db 264 ACATCTATGTTATGCTCATCTAGTAACCTTGAGAAAA 225

## RESULT 11

US-09-783-590-1239  
; Sequence 1239, Application US/09783590  
; Patent No. US20020110950A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1239  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (8)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (148)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (358)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (369)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (373)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (375)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (380)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (382)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (383)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (386)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (388)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (412)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (419)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (422)  
; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc feature  
; LOCATION: (480)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-1239

## Query Match

Best Local Similarity 7.6%; Score 33.4; DB 10; Length 491;  
Matches 58; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 301 | AGGGNTCANTTTCGGACAACTANNTCTTANAANNAATTGTCAAAAATNGGTGNCNATT | 360 |
| DB | 338 | AGGTTCCAGGATCGTCCCAAGAGTTAGNCCCNANGGTANANNCTNGNATTAGTATA   | 397 |
| QY | 361 | GAGGAAGCNAATNAGTCCCAAGAGTTAGNCCCNANGGTANANNCTNGNATTAGTATA  | 420 |
| DB | 398 | GGGGAGGGGATTCATCAAGNCCNATGTTGGTTAAACCAAGTGAATTTGGGCCAGG    | 457 |
| QY | 421 | GGAATNTAGATAAA   | 435 |
| DB | 458 | GGAATNTAGATAAA   | 472 |

## RESULT 12

US-09-942-366-4  
; Sequence 4, Application US/09942366  
; Patent No. US20020048565A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Daniel S  
; Takahara, Kazuhiko  
; Hoffman, Guy G  
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/942,366  
; FILING DATE: 29-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/240,473  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berson, Bennett J  
; REGISTRATION NUMBER: 37094  
; REFERENCE/DOCKET NUMBER: 960296.93839  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3919 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 648..3689  
; OTHER INFORMATION: /product= "human mTll protein"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-942-366-4

Query Match 7.6%; Score 33.4; DB 10; Length 3919;  
Best Local Similarity 48.7%; Pred. No. 2.8;  
Matches 76; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 6 GCGCGGCGGACTTCGCTTTTCCTCCCGCGTACGCTCGCGCTCCNNTGAGCGTGG 65  
DB 129 GTGACAGCGGATTCATCTCTCGAGCTGCGCGCGGCTTTTGGCTCAGCGCGCGC 188

QY 66 CGTACCGCGCGAGCGAGCGGTGGTGGCGATGCGTNCGCTGATGCGCGCT 125  
DB 189 GCTCGGCTCGCGCGGAGCTCTGGAGACAGCGGAGCGCGCGGAGTCCGAGCTC 248

QY 126 GCGGNGAFGNCCTCTTCATCCNCGNATNCCGA 161  
DB 249 TGTGCGAGCTGAGCGCGCGGCGCGCTCGCGCA 284

RESULT 13  
US-10-096-241-1/c  
; Sequence 1, Application US/10096241  
; Patent No. US20020127594A1  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; Busfield, Samantha J.  
; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES  
; AND USES THEREFOR  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096.241  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/699,591  
; FILING DATE: 19-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 07334/022001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2467 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 79...1893  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-096-241-1

Query Match 7.5%; Score 33.2; DB 12; Length 2467;  
Best Local Similarity 59.6%; Pred. No. 2.4;  
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 36 CGTCAGCGTCCGCGCTCCNNTGAGCTGCGCTCACCGCGCGAGCGAGCGCGGT 95  
DB 1574 CCGCAGCGCGCGCGCGCGAGTCTCTCGGAGCGCGCGCGTGGCGCGCGGC 1515

QY 96 GGTGGCGATGGCGTNCGCTGATGCGCT 124  
DB 1514 GCGCGGGGGCGCGCACTCTCGTGGT 1486

RESULT 14  
US-09-070-927A-281  
; Sequence 281, Application US/09070927A  
; Patent No. US20020120116A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Kunsch  
; Patrick J. Dillon  
; Steven Barash  
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 982  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,927A  
; FILING DATE: 04-May-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,655  
; FILING DATE: 1997-05-16  
; APPLICATION NUMBER: 60/044,031  
; FILING DATE: 1997-05-06  
; APPLICATION NUMBER: 60/066,009  
; FILING DATE: 1997-11-14  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kenley K. Hoover  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PB369  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 281:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5830 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 281:  
US-09-070-927A-281

Query Match 7.5%; Score 33.2; DB 10; Length 5830;  
Best Local Similarity 46.8%; Pred. No. 4;  
Matches 94; Conservative 1; Mismatches 105; Indels 1; Gaps 1;

QY 142 TNCATCCNGTNNCCCGACTTNCACAGCGAGGATNATGTTTCAGGACATCANGANG 201  
DB 5037 TACATTCGACGATTCCTCAGATTATCTCGAGAGGATCGTGTCCGTGACATYTCCTCA 5096

QY 202 NTGNTGTTCTGATCCCAAGCGGTCGTGACACATATACCATTTGTCACGGGTACAAG 261  
DB 5097 TTAATGGCTTAATGGGATGCTCTATCTGTAAGCAACGAACAAATCTGGATTACCGAAA 5156

QY 262 GACCAAGGNATCCNCGAANTAGAGTAAAGCTAGAGGNTCANTTTCCGGAACAAC 321  
DB 5157 GAAAAAGAAATGATATGG-TTGTAGGACCGGAAGCTCGTGGCTTTATTGTCGGCTGTCT 5215



Search completed: November 30, 2002, 04:09:42  
Job time : 63 secs







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; NAME/KEY: misc-feature
; LOCATION: (31)
; OTHER INFORMATION: n is a,c,g, or t
;
; FEATURE:
;
; NAME/KEY: misc-feature
; LOCATION: (48)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-40758

```

|    | Query Match           | 8.0%;  | Score 35;      | DB 5;      | Length 2137;                                  |
|----|-----------------------|--|----------------|------------|---|
|    | Best Local Similarity | 53.5%;   | Pred. NO. 1.6; |            |   |
|    | Matches 68;           | Conservative 0;  | Mismatches 59; | Indels 0;  | Gaps  |
| QY | 6                     | GC   | CGCGCGGCAC     | TTTCGCTTTT | CGCTCCCGCGGTCACGCGCTCCGCGGCTCCNNGTAGCGGTGG 65 |
| Db | 442                   | GAGGAGGACGACGATGACATCTCTGTGGCCCGCCGCTGCTGGGGGCTCCCGCGGCGCCCGCG 501 |                |            |   |
| QY | 66                    | GCTACACGGGGGCGGACGAGCGAGCGGTGCTGGCGATGGCGTATGCGGCGCTT 125          |                |            |   |
| Db | 502                   | GGCCGGGCCCGGGGGGCGAGGACGCGGTGGGGGCGCGCGGGCGCGCGCGCGCG 561          |                |            |   |
| QY | 126                   | GGCGNG 132   |                |            |   |
| Db | 562                   | GGCGCG 568   |                |            |   |

## RESULT 8

```

US-09-724-676-13643
; Sequence 13643, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13643
; LENGTH: 2259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-13643

```

|    | Query Match           | 7.7%   | Score 34;      | DB 5;     | Length 2259; |
|----|-----------------------|--|----------------|-----------|--------------|
|    | Best Local Similarity | 53.6%  | Pred. No. 3.3; |           |              |
|    | Matches 67;           | Conservative 0;  | Mismatches 58; | Indels 0; | Gaps 0;      |
| QY | 6                     | GGCCGCGCGCATTCGCTTTTCGTCGCCCGCTCACCGCTCGCGGGCTCCNNTGAGCGTGCG | 65             |           |              |
| DB | 438                   | GGCTCGAGGCGGCGCGCGGAGGCGCCGCGCGGGCGGCGCGGAGCGACCTGCG         | 497            |           |              |
| QY | 66                    | CGTCACCGCGCGGCGAGGCGAGGCGGTGTGTGCGGATGGCGGTTCGCTGATCGCGCGTT  | 125            |           |              |
| DB | 498                   | CGCGAAGCTCGCCCGCGAATGCGCGCGCGCGGACCGGGCTCCCGGCGCGCGCCCTA     | 557            |           |              |

## RESULT 7

```

US-09-724-676A-40758
; Sequence 40738, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40758
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```



Db 438 GCGTCGGAGCGGGCCCCCGAGCCCGCGCGGGCGCGGCGCGGAGGACCTGCG 497  
QY 66 CQTACCGCGCGAGCGAGCGAGCGGCTGTGGCGATGCGCTGCGGCGCTT 125  
Db 498 CCGCAGCGCTCCCCCGAATGGCGCGGCGCGGCGGCTCCCGCGCGCGGCCCTA 557  
QY 126 GCGCG 130  
Db 558 GCGCG 562

## RESULT 14

US-09-724-676-13642  
; Sequence 13642, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13642  
; LENGTH: 2353  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-13642

Query Match 7.7%; Score 34; DB 5; Length 2353;  
Best Local Similarity 53.6%; Pred. No. 3.4;  
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 6 GCGCGCGCGGACTTCGCTTTTCGTCGCCGCGTACGCGTCCGCGCTCCNNFTGAGCGTGG 65  
Db 438 GCGTCGGAGCGGGCGGCCCGCGAGGCCCCCGCGGGCGCGCGGAGGACCTGCG 497  
QY 66 CQTACCGCGCGAGCGAGCGGCGTGTGGCGATGCGCTGCGCTGATGCGGCGCTT 125  
Db 498 CCGCAGCGCTGCCCGCAATGGCGGCGCGGCGGCGGCTCCCGCGCGGCCCTA 557  
QY 126 GCGCG 130  
Db 558 GCGCG 562

## RESULT 15

US-09-724-676A-13642  
; Sequence 13642, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13642  
; LENGTH: 2353  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-13642

Query Match 7.7%; Score 34; DB 5; Length 2353;  
Best Local Similarity 53.6%; Pred. No. 3.4;  
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 6 GCGCGCGCGGACTTCGCTTTTCGTCGCCGCGTACGCGTCCGCGCTCCNNFTGAGCGTGG 65  
Db 438 GCGTCGGAGCGGGCGGCCCGCGAGGCCCCCGCGGGCGCGGCGGAGGACCTGCG 497  
QY 66 CQTACCGCGCGAGCGAGCGGCGTGTGGCGATGCGCTGCGCTGATGCGGCGCTT 125  
Db 498 CCGCAGCGCTGCCCGCAATGGCGGCGCGGCGGCGGCTCCCGCGCGGCCCTA 557

Qy 126 GCGCG 130  
Db 558 GCGCG 562

Search completed: November 30, 2002, 04:11:06  
Job time : 92 secs

